

Swope, Sheridan

From: Swope, Sheridan
Sent: Thursday, February 09, 2006 3:04 PM
To: Chan, Christina
Subject: FW: 08/817,997_10/714,755

Chris, May I have this rushed?--Not enough hits collected in the A_Geneseq database.

From 08/817,997, please search :

SID 2, residues 36-229, against the A_Geneseq (.rag) database only.
**Collect the top 250 hits.

Note: this sequence begins with: (N-terminus)-Gln-Leu-Gly-Ala-Ile-
and ends with: -Asp-Arg-Ile-Arg-Ala-(C-terminus)

Please let me know if you have any questions.

Thanks,
Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

See Claim 45

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Tuesday, January 31, 2006 10:25 AM
To: Swope, Sheridan
Subject: RE: 08/817,997_10/714,755

CRFA - SEQUENCE MOVED TO PUBLIC DATABASE. Your request is in. maude

-----Original Message-----

From: Swope, Sheridan
Sent: Monday, January 30, 2006 9:23 PM
To: STIC-Biotech/ChemLib
Subject: 08/817,997_10/714,755

From 08/817,997, please search and interference search:

SID 2, residues 36-229, against the NT and AA data bases.

Note: this sequence begins with: (N-terminus)-Gln-Leu-Gly-Ala-Ile-
and ends with: -Asp-Arg-Ile-Arg-Ala-(C-terminus)

Please let me know if you have any questions.

Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

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From: Swope, Sheridan
Sent: Monday, January 30, 2006 9:23 PM
To: STIC-Biotech/ChemLib
Subject: 08/817,997_10/714,755

From 08/817,997, please search and interference search:

SID 2, residues 36-229, against the NT and AA data bases.

Note: this sequence begins with: (N-terminus)-Gln-Leu-Gly-Ala-Ile-
and ends with: -Asp-Arg-Ile-Arg-Ala-(C-terminus)

Please let me know if you have any questions.

Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 178059

TO: Sheridan Swope
Location: rem/2B71/3C70
Art Unit: 1656
Wednesday, February 08, 2006
Case Serial Number: 08/817997

From: Kristine
Location: Biotech-Chem Library
REM-1B69
Phone: (571)272-4161

Kristine.Hensle@uspto.gov

Search Notes

Examiner Swope,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:48:19 ; Search time 199 Seconds
(without alignments)
428.339 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229
Perfect score: 996
Sequence: 1 QIGAIENGLESGSANACPD.....SYTIARGEARFLDRIRA 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	996	100.0	246	2	AAR95051 H. insole
2	991	99.5	194	5	AAM48435 Wild-type
3	991	99.5	194	6	Aae34646 Humicola
4	988	99.2	194	3	AAB13715 H. insole
5	987	99.1	194	3	AAB13706 H. insole
6	987	99.1	194	5	ABB76837 Mutant Hu
7	987	99.1	194	5	ABB76844 Mutant Hu
8	987	99.1	194	5	ABB76838 Mutant Hu
9	987	99.1	194	6	Aae34652 Humicola
10	985	98.9	194	3	AAB13707 H. insole
11	985	98.9	194	5	ABB76839 Mutant Hu
12	985	98.9	194	6	Aae34653 Humicola
13	984	98.8	194	3	AAB13703 H. insole
14	984	98.8	194	6	Aae34649 Humicola
15	983	98.7	194	3	AAB13704 H. insole
16	983	98.7	194	5	ABB76845 Mutant Hu
17	983	98.7	194	6	Aae34650 Humicola
18	982	98.6	194	3	AAB13705 H. insole
19	982	98.6	194	3	AAB13711 H. insole
20	982	98.6	194	5	ABB76829 Mutant Hu
21	982	98.6	194	6	Aae34651 Humicola
22	982	98.6	194	6	Aae34657 Humicola
23	981	98.5	194	3	AAB13710 H. insole
24	981	98.5	194	5	ABB76834 Mutant Hu

25	981	98.5	194	6	AAE34656	Aae34656 Humicola
26	980	98.4	194	5	ABB76831	Abb76831 Mutant Hu
27	979	98.3	194	3	AAB13717	Aab13717 H. insole
28	977	98.1	194	3	AAB13716	Aab13716 H. insole
29	976	98.0	194	3	AAB13709	Aab13709 H. insole
30	976	98.0	194	5	ABB76830	Abb76830 Mutant Hu
31	976	98.0	194	6	AAE34655	Aae34655 Humicola
32	975	97.9	194	5	ABB76836	Abb76836 Mutant Hu
33	975	97.9	194	5	ABB76846	Abb76846 Mutant Hu
34	975	97.9	194	5	ABB76843	Abb76843 Mutant Hu
35	974	97.8	194	3	AAB13708	Aab13708 H. insole
36	974	97.8	194	6	AAE34654	Aae34654 Humicola
37	970	97.4	194	5	ABB76832	Abb76832 Mutant Hu
38	970	97.4	194	5	ABB76828	Abb76828 Mutant Hu
39	969	97.3	194	3	AAB13718	Aab13718 H. insole
40	969	97.3	194	5	ABB76857	Abb76857 Mutant Hu
41	969	97.3	194	6	AAE34660	Aae34660 Humicola
42	968	97.2	194	5	ABB76835	Abb76835 Mutant Hu
43	968	97.2	194	5	ABB76827	Abb76827 Mutant Hu
44	966	97.0	194	3	AAB13719	Aab13719 H. insole
45	966	97.0	194	6	AAE34659	Aae34659 Humicola

RESULT 1

AAAR95051	17-DEC-1996 (first entry)	Location/Qualifiers
XX	AAAR95051 standard; protein; 246 AA.	1..35
AC	AAAR95051;	/label= signal_peptide
XX		36..246
DT		/label= mature_protein
XX		
DE	H. insolens lipase.	
XX	lipase; detergent; dishwashing; laundry; short-chain lipid.	
XX	Humicola insolens.	
XX		
FH	Key	
FT	Peptide	
FT	Protein	
XX		
PN	WO9613580-A1.	
XX		
PD	09-MAY-1996.	
XX		
PF	26-OCT-1995; 95WO-DK000427.	
XX		
PR	26-OCT-1994; 94DK-00001240.	
XX	(NOVO) NOVO-NORDISK AS.	
PI	Sandal T, Kauppinen S, Kofod LV;	
XX		
DR	WPI; 1996-239493/24.	
DR	N-ESDB; AAT29401.	
XX		
PT	Isolated DNA encoding lipolytic enzyme - derived from Humicola insolens	
PT	DSM1800, used partic. as detergent additive for laundry and dishwashing	
XX		
PS	compsns.	
XX		
XX	Disclosure; Page 52; 63pp; English.	
XX		
CC	The present sequence is that of an enzyme with lipolytic activity,	
CC	derived from Humicola insolens DSM1800. The enzyme has a mol. wt. of	
CC	about 20-21 kDa, a pi in the range of 709, a pH optimum of about 8 and	
CC	has specificity towards short-chain lipid substrates. It can be used as a	
CC	detergent additive, partic. in compsns. for laundry washing or	
CC	dishwashing	

need more 80 claim 45

XX SQ Sequence 246 AA;
 Query Match 100.0%; Score 996; DB 2; Length 246;
 Best Local Similarity 100.0%; Pred. No. 2.9e-98;
 Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
 DB 36 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 95
 QY 61 PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVAGGYSOGAALIAAAVSELG 120
 DB 96 PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVAGGYSOGAALIAAAVSELG 155
 QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVFNCNVGDAVCTGTLITPAHLSYITIEA 180
 DB 156 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVFNCNVGDAVCTGTLITPAHLSYITIEA 215
 QY 181 RGEAARFLDRIRA 194
 DB 216 RGEAARFLDRIRA 229

RESULT 2
 AAM48435
 ID AAM48435 standard; protein; 194 AA.
 XX AC AAM48435;
 XX DT 29-AUG-2003 (revised)
 DT 25-JUN-2002 (first entry)
 XX DE Wild-type Humicola insolens mature cutinase.
 XX KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin.
 XX OS Humicola insolens; strain DSM 1800.
 XX PN WO200192502-A1.
 XX PD 06-DEC-2001.
 XX PF 22-MAY-2001; 2001WO-DK000350.
 XX PR 02-JUN-2000; 2000DK-00000861.
 PR 23-OCT-2000; 2000DK-00001577.
 PR 24-NOV-2000; 2000DK-00001772.
 PR 19-JAN-2001; 2001DK-00000100.
 XX PA (NOVO) NOVOZYMES AS.
 XX SV Svendsen A, Glad SOS, Fukuyama S, Matsui T;
 XX WI; 2002-216714/27.
 XX PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
 PT oligomers of poly(ethylene terephthalate), comprises a substitution of
 PT amino acid residues corresponding to positions of Humicola insolens
 PT cutinase.
 XX PS Disclosure; Page 36; 41pp; English.
 XX CC The present sequence is the wild-type mature cutinase from Humicola
 CC insolens strain DSM 1800, which was used to generate mutant cutinases
 CC (see ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic enzymes
 CC capable of hydrolysing the substrate cutin. The mutant cutinases have
 CC improved thermostability, and are used for enzymatic hydrolysis of cyclic
 CC oligomers of poly(ethylene terephthalate), e.g. in the finishing of yarn
 CC or fabric from poly(ethylene terephthalate) fibers. (Updated on 29-AUG-
 CC 2003 to standardise OS field)
 XX SQ Sequence 194 AA;

Query Match 99.5%; Score 991; DB 5; Length 194;
 Best Local Similarity 99.5%; Pred. No. 7.1e-98;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
 QY 61 PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVAGGYSOGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVAGGYSOGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVFNCNVGDAVCTGTLITPAHLSYITIEA 180
 DB 121 AVKEQVKGVALFGYTONLQNRGGIANYPRTKVFNCNVGDAVCTGTLITPAHLSYITIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194

RESULT 3
 AAE34646
 ID AAE34646 standard; protein; 194 AA.
 XX AC AAE34646;
 XX DT 14-MAY-2003 (first entry)
 XX DE Humicola insolens cutinase protein.
 XX KW Lipolytic enzyme; cutinase; lipase; paper; enzyme.
 XX OS Humicola insolens.
 XX PN WO200295127-A2.
 XX PD 28-NOV-2002.
 XX PF 17-MAY-2002; 2002WO-DK000326.
 XX PR 21-MAY-2001; 2001DK-00000813.
 XX PA (NOVO) NOVOZYMES AS.
 XX PI Borch K, Lund H, Sharyo M, Sakaguchi H, Pedersen HH;
 PI Fitzhenry JW;
 XX WI; 2003-156764/15.
 XX PT Making paper comprises preparing pulp from recycled paper, and treating
 PT pulp with a lipolytic enzyme, which is able to hydrolyze a polymer
 PT comprising a vinyl acetate monomer.
 XX PS Disclosure; Page 36-37; 40pp; English.
 XX CC The invention relates to the use of certain lipolytic enzymes such as
 CC cutinases and lipases in the manufacture of paper and paper products from
 CC recycled paper. The invention also relates to a method of making paper
 CC which involves preparing a pulp recycled paper, treating the pulp with a
 CC lipolytic enzyme which is able to hydrolyse a polymer comprising vinyl
 CC acetate monomer and making paper from the treated pulp. The method is
 CC used for making paper from recycled paper. The method of the invention
 CC provides stickies control and/or de-inking. The present sequence is
 CC Humicola insolens cutinase protein
 XX SQ Sequence 194 AA;

Query Match 99.5%; Score 991; DB 6; Length 194;
 Best Local Similarity 99.5%; Pred. No. 7.1e-98;
 Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLGAIEIENGLESGSANACPDALLIFARGSTEPGNMGITVGPALANGLESHERINWIQGVGG 60
 Db 1 QLGAIEIENGLESGSANACPDALLIFARGSTEPGNMGITVGPALANGLESHERINWIQGVGG 60
 QY 61 PYDAALATNPLPRGTQSANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
 Db 61 PYDAALATNPLPRGTQSANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALLFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGLTIITPAHLSYTTIEA 180
 Db 121 AVKEQVKGVALLFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGLTIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIR 194
 Db 181 RGEAARFLDRIR 194
 RESULT 4
 AAB13715
 ID AAB13715 standard; protein; 194 AA.
 AC AAB13715;
 XX
 DT 17-NOV-2000 (first entry)
 XX
 DE H. insolens mutant cutinase, E179Q substitution.
 XX
 KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX
 OS Humicola insolens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 179 /note= "Wild-type Glu substituted by Gln"
 FT
 XX WO200034450-A1.
 PN
 PD 15-JUN-2000.
 XX
 PF 03-DEC-1999; 99WO-DK000678.
 XX
 PR 04-DEC-1998; 98DK-00001604.
 PR 09-DEC-1998; 98US-0111591P.
 PR 09-MAR-1999; 99DK-00000330.
 PR 16-MAR-1999; 99US-0124671P.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PI Abo M, Fukuyama S, Svendsen A, Matsui T;
 XX
 DR WPI; 2000-482424/42.
 XX
 PT Thermostable variant of parent fungal cutinase useful for dyeing
 PT polyester yarn or fabric, comprises substitution of amino acid residues
 PT at predetermined positions from the N-terminal amino acid.
 XX
 PS Example 1; Page; 79pp; English.
 XX
 CC Site-directed mutagenesis was carried out on wild-type Humicola insolens
 CC cutinase, to produce the present sequence. The introduced substitution
 CC improves the thermostability of the cutinase enzyme. Cutinases are
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
 CC thermostability are useful since they can withstand higher processing
 CC temperatures. Note: the present sequence is not shown in the
 CC specification but is derived from the H. insolens wild-type cutinase
 CC sequence given in SEQ ID 2 of patent: US 5,827,719

SQ Sequence 194 AA;
 Query Match 99.2%; Score 988; DB 3; Length 194;
 Best Local Similarity 99.0%; Pred. No. 1.5e-97;
 Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLGAIEIENGLESGSANACPDALLIFARGSTEPGNMGITVGPALANGLESHERINWIQGVGG 60
 Db 1 QLGAIEIENGLESGSANACPDALLIFARGSTEPGNMGITVGPALANGLESHERINWIQGVGG 60
 QY 61 PYDAALATNPLPRGTQSANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
 Db 61 PYDAALATNPLPRGTQSANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALLFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGLTIITPAHLSYTTIEA 180
 Db 121 AVKEQVKGVALLFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGLTIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIR 194
 Db 181 RGEAARFLDRIR 194
 RESULT 5
 AAB13706
 ID AAB13706 standard; protein; 194 AA.
 XX
 AC AAB13706;
 XX
 DT 17-NOV-2000 (first entry)
 XX
 DE H. insolens mutant cutinase, E47K substitution.
 XX
 KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX
 OS Humicola insolens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 47 /note= "Wild-type Glu substituted by Lys"
 FT
 XX WO200034450-A1.
 PN
 PD 15-JUN-2000.
 XX
 PF 03-DEC-1999; 99WO-DK000678.
 XX
 PR 04-DEC-1998; 98DK-00001604.
 PR 09-DEC-1998; 98US-0111591P.
 PR 09-MAR-1999; 99DK-00000330.
 PR 16-MAR-1999; 99US-0124671P.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 PI Abo M, Fukuyama S, Svendsen A, Matsui T;
 XX
 DR WPI; 2000-482424/42.
 XX
 PT Thermostable variant of parent fungal cutinase useful for dyeing
 PT polyester yarn or fabric, comprises substitution of amino acid residues
 PT at predetermined positions from the N-terminal amino acid.
 XX
 PS Claim 16; Page; 79pp; English.
 XX
 CC Site-directed mutagenesis was carried out on wild-type Humicola insolens
 CC cutinase, to produce the present sequence. The introduced substitution
 CC improves the thermostability of the cutinase enzyme. Cutinases are
 CC lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from

CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
 CC thermostability are useful since they can withstand higher processing
 CC temperatures. Note: the present sequence is not shown in the
 CC specification but is derived from the H. insolens wild-type cutinase
 CC sequence given in SEQ ID 2 of patent: US 5,827,719
 XX
 XX Sequence 194 AA;
 SQ
 Query Match 99.1%; Score 987; DB 3; Length 194;
 Best Local Similarity 99.0%; Pred. No. 1.9e-97;
 Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLGAENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESHIRNIWIOGVGG 60
 DB 1 QLGAENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESHIRNIWIOGVGG 60
 QY 61 PYDAALATNLFPRGTSGQANIDEGKRLPALANQKCPNTPVVAGYSQGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSGQANIDEGKRLPALANQKCPNTPVVAGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRERTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTONLQNRGGIANYPRERTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
 QY 181 RGEAARFLRDRIRA 194
 DB 181 RGEAARFLRDRIRA 194
 RESULT 6
 ID ABB76837 standard; protein; 194 AA.
 AC ABB76837;
 DT 25-JUN-2002 (first entry)
 DE Mutant Humicola insolens mature cutinase #11.
 KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
 XX Humicola insolens; strain DSM 1800.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 164 /note= "Wild-type Thr substituted by Ser"
 FT WO200192502-A1.
 PN 06-DEC-2001.
 XX 22-MAY-2001; 2001WO-DK000350.
 PF 02-JUN-2000; 2000DK-00000861.
 PR 23-OCT-2000; 2000DK-00001577.
 PR 24-NOV-2000; 2000DK-00001772.
 PR 19-JAN-2001; 2001DK-00000100.
 XX (NOVO) NOVOZYMES AS.
 XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;
 XX WPI; 2002-216714/27.
 DR Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
 XX oligomers of poly(ethylene terephthalate), comprises a substitution of
 PT amino acid residues corresponding to positions of Humicola insolens
 PT cutinase.
 XX Claim 8; Page; 41pp; English.
 PS
 XX The present invention relates to wild-type mature cutinase from Humicola
 CC

CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
 CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
 CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
 CC have improved thermostability, and are used for enzymatic hydrolysis of
 CC cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing
 CC of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the
 CC present sequence is not shown in the specification, but is derived from
 CC the wild-type cutinase sequence shown on page 36
 XX
 XX Sequence 194 AA;
 SQ
 Query Match 99.1%; Score 987; DB 5; Length 194;
 Best Local Similarity 99.0%; Pred. No. 1.9e-97;
 Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLGAENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESHIRNIWIOGVGG 60
 DB 1 QLGAENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESHIRNIWIOGVGG 60
 QY 61 PYDAALATNLFPRGTSGQANIDEGKRLPALANQKCPNTPVVAGYSQGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSGQANIDEGKRLPALANQKCPNTPVVAGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRERTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTONLQNRGGIANYPRERTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
 QY 181 RGEAARFLRDRIRA 194
 DB 181 RGEAARFLRDRIRA 194
 RESULT 7
 ID ABB76844 standard; protein; 194 AA.
 AC ABB76844;
 DT 25-JUN-2002 (first entry)
 DE Mutant Humicola insolens mature cutinase #18.
 KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
 XX Humicola insolens; strain DSM 1800.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 130 /note= "Wild-type Arg substituted by Val"
 FT WO200192502-A1.
 PN 06-DEC-2001.
 XX 22-MAY-2001; 2001WO-DK000350.
 PF 02-JUN-2000; 2000DK-00000861.
 PR 23-OCT-2000; 2000DK-00001577.
 PR 24-NOV-2000; 2000DK-00001772.
 PR 19-JAN-2001; 2001DK-00000100.
 XX (NOVO) NOVOZYMES AS.
 XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;
 XX WPI; 2002-216714/27.
 DR Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
 XX oligomers of poly(ethylene terephthalate), comprises a substitution of
 PT amino acid residues corresponding to positions of Humicola insolens
 PT cutinase.
 XX

PS Claim 8; Page; 4lpp; English.

XX The present invention relates to wild-type mature cutinase from Humicola

CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant

CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic

CC enzymes capable of hydrolyzing the substrate cutin. The mutant cutinases

CC have improved thermostability, and are used for enzymatic hydrolysis of

CC cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing

CC of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the

CC present sequence in not shown in the specification, but is derived from

CC the wild-type cutinase sequence shown on page 36

XX Sequence 194 AA;

SQ

Query Match 99.1%; Score 987; DB 5; Length 194;

Best Local Similarity 99.0%; Pred. No. 1.9e-97;

Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60

DB 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60

QY 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGYSQGAALIAAAVSELG 120

DB 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGYSQGAALIAAAVSELG 120

QY 121 AVKEQKGVVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

DB 121 AVKEQKGVVLFYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

QY 181 RGEAARFLDRIRA 194

DB 181 RGEAARFLDRIRA 194

RESULT 8

ABB76838

ID ABB76838 standard; protein; 194 AA.

XX ABB76838;

XX

DT 25-JUN-2002 (first entry)

XX

DE Mutant Humicola insolens mature cutinase #12.

XX

KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.

XX

OS Humicola insolens; strain DSM 1800.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 174 /note= "Wild-type Leu substituted by Phe"

FT

XX WO200192502-A1.

XX

PN

PD 06-DEC-2001.

XX

XX 22-MAY-2001; 2001WO-DK000350.

XX

XX 02-JUN-2000; 2000DK-00000861.

PR 23-OCT-2000; 2000DK-00001577.

PR 24-NOV-2000; 2000DK-00001772.

PR 19-JAN-2001; 2001DK-00000100.

XX

XX (NOVO) NOVOZYMES AS.

XX

XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;

XX

DR WPI; 2002-216714/27.

XX

PT Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic

PT oligomers of poly(ethylene terephthalate), comprises a substitution of

PT

PT amino acid residues corresponding to positions of Humicola insolens

PT cutinase.

XX Claim 8; Page; 4lpp; English.

XX The present invention relates to wild-type mature cutinase from Humicola

CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant

CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic

CC enzymes capable of hydrolyzing the substrate cutin. The mutant cutinases

CC have improved thermostability, and are used for enzymatic hydrolysis of

CC cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing

CC of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the

CC present sequence in not shown in the specification, but is derived from

CC the wild-type cutinase sequence shown on page 36

XX Sequence 194 AA;

SQ

Query Match 99.1%; Score 987; DB 5; Length 194;

Best Local Similarity 99.0%; Pred. No. 1.9e-97;

Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60

DB 1 QLGAIENGLESGSANACPDAILIFARGSTEPGNMGITVGPALANGLESIRNIWIQVGG 60

QY 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGYSQGAALIAAAVSELG 120

DB 61 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGYSQGAALIAAAVSELG 120

QY 121 AVKEQKGVVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

DB 121 AVKEQKGVVLFYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

QY 181 RGEAARFLDRIRA 194

DB 181 RGEAARFLDRIRA 194

RESULT 9

AAE34652

ID AAE34652 standard; protein; 194 AA.

XX AAE34652;

XX

DT 14-MAY-2003 (first entry)

XX

DE Humicola insolens cutinase mutant protein #4.

XX

KW Lipolytic enzyme; cutinase; lipase; paper; enzyme; mutant; mutein.

XX

OS Humicola insolens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 47 /note= "Wild-type Glu substituted with Lys"

FT

XX WO200295127-A2.

XX

XX 28-NOV-2002.

XX

XX 17-MAY-2002; 2002WO-DK000326.

XX

XX 21-MAY-2001; 2001DK-00000813.

XX

XX (NOVO) NOVOZYMES AS.

XX

XX Borch K, Lund H, Sharyo M, Sakaguchi H, Pedersen HH;

PI Fitzhenry JW;

XX

XX WPI; 2003-156764/15.

XX

XX Making paper comprises preparing pulp from recycled paper, and treating

PT pulp with a lipolytic enzyme, which is able to hydrolyze a polymer
 XX comprising a vinyl acetate monomer.
 PS Disclosure; Page; 40pp; English.
 XX
 CC The invention relates to the use of certain lipolytic enzymes such as
 CC cutinases and lipases in the manufacture of paper and paper products from
 CC recycled paper. The invention also relates to a method of making paper
 CC which involves preparing a pulp recycled paper, treating the pulp with a
 CC lipolytic enzyme which is able to hydrolyse a polymer comprising vinyl
 CC acetate monomer and making paper from the treated pulp. The method is
 CC used for making paper from recycled paper. The method of the invention
 CC provides stickies control and/or de-inking. The present sequence is
 CC Humicola insolens cutinase mutant protein (B47K). Note: This sequence is
 CC not shown in the specification but is derived from Humicola insolens
 CC cutinase protein shown as SEQ ID NO: 1 in pages 36-37 of the
 CC specification (AAE34646)
 XX
 XX Sequence 194 AA;
 SQ
 Query Match 99.1%; Score 987; DB 6; Length 194;
 Best Local Similarity 99.0%; Pred. No. 1.9e-97;
 Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQVGG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQVGG 60
 QY 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRERTKVCNVDGAVCTGTLIITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRERTKVCNVDGAVCTGTLIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194
 RESULT 10
 AAB13707
 ID AAB13707 standard; protein; 194 AA.
 XX
 AC AAB13707;
 XX
 XX 17-NOV-2000 (first entry)
 DT
 DE H. insolens mutant cutinase, E179X substitution.
 XX
 KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX
 OS Humicola insolens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 179
 FT /note= "Wild-type Glu substituted by Asn or Gln"
 XX
 XX WO200034450-A1.
 PN
 XX
 XX 15-JUN-2000.
 PD
 XX
 XX 03-DEC-1999; 99WO-DK000678.
 PP
 XX
 PR 04-DEC-1998; 98DK-00001604.
 PR 09-DEC-1998; 98US-0111591P.
 PR 09-MAR-1999; 99DK-00000330.
 PR 16-MAR-1999; 99US-0124671P.
 PR

PA (NOVO) NOVO-NORDISK AS.
 XX
 PI Abo M, Fukuyama S, Svendsen A, Matsui T;
 XX
 DR WPI; 2000-482424/42.
 XX
 XX Thermostable variant of parent fungal cutinase useful for dyeing
 PT polyester yarn or fabric, comprises substitution of amino acid residues
 PT at predetermined positions from the N-terminal amino acid.
 XX
 XX Claim 16; Page; 79pp; English.
 PS
 XX Site-directed mutagenesis was carried out on wild-type Humicola insolens
 CC cutinase, to produce the present sequence. The introduced substitution
 CC improves the thermostability of the cutinase enzyme. Cutinases are
 CC lipolytic enzymes capable of hydrolysis of the substrate cutin. Cutinase
 CC may be used in the enzymatic hydrolysis of cyclic oligomers of
 CC poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from
 CC poly(ethylene terephthalate) fibers. Cutinase variants with improved
 CC thermostability are useful since they can withstand higher processing
 CC temperatures. Note: the present sequence is not shown in the
 CC specification but is derived from the H. insolens wild-type cutinase
 CC sequence given in SEQ ID 2 of patent: US 5,827,719
 XX
 XX Sequence 194 AA;
 SQ
 Query Match 98.9%; Score 985; DB 3; Length 194;
 Best Local Similarity 99.0%; Pred. No. 3.2e-97;
 Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQVGG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQVGG 60
 QY 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRERTKVCNVDGAVCTGTLIITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRERTKVCNVDGAVCTGTLIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIRA 194
 DB 181 RGEAARFLDRIRA 194
 RESULT 11
 ABB76839
 ID ABB76839 standard; protein; 194 AA.
 XX
 AC ABB76839;
 XX
 XX 25-JUN-2002 (first entry)
 DT
 XX
 DE Mutant Humicola insolens mature cutinase #13.
 XX
 KW Cutinase; enzyme; EC 3.1.1.74; lipolytic enzyme; cutin; mutant; mutein.
 XX
 OS Humicola insolens; strain DSM 1800.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 49
 FT /note= "Wild-type His substituted by Tyr"
 XX
 XX WO200192502-A1.
 PN
 XX
 XX 06-DEC-2001.
 PD
 XX
 XX 22-MAY-2001; 2001WO-DK000350.
 PF
 XX
 XX 02-JUN-2000; 2000DK-00000861.
 PR

PR 23-OCT-2000; 2000DK-00001577.
 PR 24-NOV-2000; 2000DK-00001772.
 PR 19-JAN-2001; 2001DK-00000100.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 XX Svendsen A, Glad SOS, Fukuyama S, Matsui T;
 PI WPI; 2002-216714/27.
 XX
 XX Variant of parent fungal cutinase for enzymatic hydrolysis of cyclic
 PT oligomers of poly(ethylene terephthalate), comprises a substitution of
 PT amino acid residues corresponding to positions of Humicola insolens
 PT cutinase.
 XX
 PS Claim 8; Page; 41pp; English.
 XX
 CC The present invention relates to wild-type mature cutinase from Humicola
 CC insolens strain DSM 1800 (AAM48435), which was used to generate mutant
 CC cutinases (ABB76827-ABB76857). Cutinases (EC 3.1.1.74) are lipolytic
 CC enzymes capable of hydrolysing the substrate cutin. The mutant cutinases
 CC have improved thermostability, and are used for enzymatic hydrolysis of
 CC cyclic oligomers of poly(ethylene terephthalate), e.g. in the finishing
 CC of yarn or fabric from poly(ethylene terephthalate) fibers. Note: the
 CC present sequence in not shown in the specification, but is derived from
 CC the wild-type cutinase sequence shown on page 36
 XX
 SQ Sequence 194 AA;
 Query Match 98.9%; Score 985; DB 5; Length 194;
 Best Local Similarity 99.0%; Pred. No. 3.2e-97;
 Matches 192; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGG 60
 QY 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGYSQGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRRTKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRRTKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIR 194
 DB 181 RGEAARFLDRIR 194
 RESULT 12
 AAE34653
 ID AAE34653 standard; protein; 194 AA.
 XX
 AC AAE34653;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Humicola insolens cutinase mutant protein #5.
 XX
 KW Lipolytic enzyme; cutinase; lipase; paper; enzyme; mutant; mutein.
 XX
 OS Humicola insolens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 179
 FT /note: "Wild-type Glu substituted with Xaa where Xaa =
 FT Asn, Gln"
 XX
 XX WO200295127-A2.
 PN
 XX 28-NOV-2002.
 PD

XX 17-MAY-2002; 2002WO-DK000326.
 XX
 PR 21-MAY-2001; 2001DK-00000813.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 XX Borch K, Lund H, Sharyo M, Sakaguchi H, Pedersen HH;
 PI Fitzhenry JW;
 XX
 XX WPI; 2003-156764/15.
 DR
 XX Making paper comprises preparing pulp from recycled paper, and treating
 PT pulp with a lipolytic enzyme, which is able to hydrolyze a polymer
 PT comprising a vinyl acetate monomer.
 PT
 XX Disclosure; Page; 40pp; English.
 PS
 XX The invention relates to the use of certain lipolytic enzymes such as
 CC cutinases and lipases in the manufacture of paper and paper products from
 CC recycled paper. The invention also relates to a method of making paper
 CC which involves preparing a pulp recycled paper, treating the pulp with a
 CC lipolytic enzyme which is able to hydrolyse a polymer comprising vinyl
 CC acetate monomer and making paper from the treated pulp. The method is
 CC used for making paper from recycled paper. The method of the invention
 CC provides stickies control and/or de-inking. The present sequence is
 CC Humicola insolens cutinase mutant protein (S179N/Q). Note: This sequence
 CC is not shown in the specification but is derived from Humicola insolens
 CC cutinase protein shown as SEQ ID NO: 1 in pages 36-37 of the
 CC specification (AAE34646)
 XX
 SQ Sequence 194 AA;
 Query Match 98.9%; Score 985; DB 6; Length 194;
 Best Local Similarity 99.0%; Pred. No. 3.2e-97;
 Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGG 60
 DB 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVGG 60
 QY 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGYSQGAALIAAAVSELG 120
 DB 61 PYDAALATNLFPRGTSGQANIDEGKRLFALANQKCPNTPVAGYSQGAALIAAAVSELG 120
 QY 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRRTKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
 DB 121 AVKEQVKGVALFGYTQNLQNRGGIANYPRRTKVFNCVGDVCTGLTIITPAHLSYTTIEA 180
 QY 181 RGEAARFLDRIR 194
 DB 181 RGEAARFLDRIR 194
 RESULT 13
 AAB13703
 ID AAB13703 standard; protein; 194 AA.
 XX
 AC AAB13703;
 XX
 DT 17-NOV-2000 (first entry)
 XX
 DE H. insolens mutant cutinase, R51P substitution.
 XX
 KW Site directed mutagenesis; cutinase; mutant; mutein; substitution;
 KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
 KW protein co-ordinate.
 XX
 OS Humicola insolens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 51

FT XX /note= "wild-type Arg substituted by Pro"

PN WO200034450-A1.

XX 15-JUN-2000.

XX 03-DEC-1999; 99WO-DK000678.

XX 04-DEC-1998; 98DK-00001604.

PR 09-DEC-1998; 98US-0111591P.

PR 09-MAR-1999; 99DK-00000330.

PR 16-MAR-1999; 99US-0124671P.

XX (NOVO) NOVO-NORDISK AS.

XX Abo M, Fukuyama S, Svendsen A, Matsui T;

PI WPI; 2000-482424/42.

XX Thermostable variant of parent fungal cutinase useful for dyeing polyester yarn or fabric, comprises substitution of amino acid residues at predetermined positions from the N-terminal amino acid.

PT Claim 16; Page; 79pp; English.

XX Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing temperatures. Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719

XX Sequence 194 AA;

Query Match 98.8%; Score 984; DB 3; Length 194;
Best Local Similarity 99.0%; Pred. No. 4e-97;
Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVG 60
Db 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVG 60

Qy 61 PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
Db 61 PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120

Qy 121 AVKEQKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180
Db 121 AVKEQKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

Qy 181 RGEAARFLDRIRA 194
Db 181 RGEAARFLDRIRA 194

RESULT 14
AAE34649
ID AAE34649 standard; protein; 194 AA.
XX AAE34649;
XX 14-MAY-2003 (first entry)
XX Humicola insolens cutinase mutant protein #1.
DE Lipolytic enzyme; cutinase; lipase; paper; enzyme; mutant; mutein.
KW Humicola insolens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 51 /note= "Wild-type Arg substituted with Pro"

XX WO200295127-A2.

XX 28-NOV-2002.

XX 17-MAY-2002; 2002WO-DK000326.

XX 21-MAY-2001; 2001DK-00000813.

XX (NOVO) NOVOZYMES AS.

XX Borch K, Lund H, Sharyo M, Sakaguchi H, Pedersen HH;
PI Fitzhenry JW;

XX WPI; 2003-156764/15.

XX Making paper comprises preparing pulp from recycled paper, and treating pulp with a lipolytic enzyme, which is able to hydrolyze a polymer comprising a vinyl acetate monomer.

PT Disclosure; Page; 40pp; English.

XX The invention relates to the use of certain lipolytic enzymes such as cutinases and lipases in the manufacture of paper and paper products from recycled paper. The invention also relates to a method of making paper which involves preparing a pulp recycled paper, treating the pulp with a lipolytic enzyme which is able to hydrolyse a polymer comprising vinyl acetate monomer and making paper from the treated pulp. The method is used for making paper from recycled paper. The method of the invention provides stickies control and/or de-inking. The present sequence is Humicola insolens cutinase mutant protein (R51P). Note: This sequence is not shown in the specification but is derived from Humicola insolens cutinase protein shown as SEQ ID NO: 1 in pages 36-37 of the specification (AAE34646)

XX Sequence 194 AA;

Query Match 98.8%; Score 984; DB 6; Length 194;
Best Local Similarity 99.0%; Pred. No. 4e-97;
Matches 192; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVG 60
Db 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIOGVG 60

Qy 61 PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
Db 61 PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120

Qy 121 AVKEQKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180
Db 121 AVKEQKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLLITPAHLSYTIEA 180

Qy 181 RGEAARFLDRIRA 194
Db 181 RGEAARFLDRIRA 194

RESULT 15
AAE34649
ID AAE34649 standard; protein; 194 AA.
XX AAE34649;
XX 17-NOV-2000 (first entry)
XX H. insolens mutant cutinase, E6X/Li38I substitution.

KW Site directed mutagenesis: cutinase; mutant; mutein; substitution;
KW thermostability; enzyme; lipolytic; fabric finishing; yarn;
KW protein co-ordinate.

XX Humicola insolens.
OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 6 /note= "Wild-type Glu substituted by Asn or Gln"

FT FT

FT Misc-difference 138 /note= "Wild-type Leu substituted by Ile"

XX FT

XX WO200034450-A1.

XX XX

XX 15-JUN-2000.

XX 03-DEC-1999; 99WO-DK000678.

XX 04-DEC-1998; 98DK-00001604.

PR 09-DEC-1998; 98US-0111591P.

PR 09-MAR-1999; 99DK-00000330.

PR 16-MAR-1999; 99US-0124671P.

XX (NOVO) NOVO-NORDISK AS.

PI Abo M, Fukuyama S, Svendsen A, Matsui T;
WPI; 2000-482424/42.

XX Claim 16; Page; 79pp; English.

XX Site-directed mutagenesis was carried out on wild-type Humicola insolens cutinase, to produce the present sequence. The introduced substitution improves the thermostability of the cutinase enzyme. Cutinases are lipolytic enzymes capable of hydrolysing the substrate cutin. Cutinase may be used in the enzymatic hydrolysis of cyclic oligomers of poly(ethylene terephthalate) e.g. in the finishing of yarn or fabric from poly(ethylene terephthalate) fibers. Cutinase variants with improved thermostability are useful since they can withstand higher processing temperatures. Note: the present sequence is not shown in the specification but is derived from the H. insolens wild-type cutinase sequence given in SEQ ID 2 of patent: US 5,827,719

XX Sequence 194 AA;

Query Match 98.7%; Score 983; DB 3; Length 194;
Best Local Similarity 98.5%; Pred. No. 5.2e-97;
Matches 191; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGESHIRNIWIOQVGG 60
DB 1 QLGAIENGLESANACPDAILIFARGSTPGNMGITVGPALANGESHIRNIWIOQVGG 60

OY 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVGYSQGAALIAAAVSELG 120
DB 61 PYDAALATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVGYSQGAALIAAAVSELG 120

OY 121 AVKEQVKGVALFGYTNLONRGIANYPRTKVCNVDGAVCTGLIITPAHLSYTIEA 180
DB 121 AVKEQVKGVALFGYTNLONRGIANYPRTKVCNVDGAVCTGLIITPAHLSYTIEA 180

OY 181 RGEARFLDRIRA 194
DB 181 RGEARFLDRIRA 194

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:52:09 ; Search time 43 Seconds
(without alignments)
434.094 Million cell updates/sec

Title: us-08-817-997-2_copy_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESGSANACPD.....SYTIEARGEARFLDRIRA 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	593.5	59.6	228	1 S20448	cutinase (EC 3.1.-)
2	576	57.8	224	1 B27451	cutinase (EC 3.1.-)
3	564	56.6	223	1 S21427	cutinase - fungus
4	550.5	55.3	228	1 A27451	cutinase (EC 3.1.-)
5	545	54.7	230	1 UVFUS	cutinase (EC 3.1.-)
6	189.5	19.0	217	2 F70756	probable cutinase
7	188.5	18.9	219	2 A70734	probable cutinase
8	178	17.9	226	2 A70565	probable cutinase
9	167.5	16.8	247	2 H70564	probable cutinase
10	115.5	11.6	187	2 E70796	probable cutinase
11	98	9.8	174	2 G70987	probable cutinase
12	96	9.6	336	2 F70887	hypothetical prote
13	89.5	9.0	420	2 T35575	hypothetical prote
14	88	8.8	1293	2 E85557	enterobactin synth
15	88	8.8	1293	2 A90707	enterobactin synth
16	88	8.8	1356	2 T18521	beta transducin-li
17	88	8.8	3355	2 E83641	probable hemagglut
18	87	8.7	336	2 C86921	conserved hypothet
19	87	8.7	892	2 S76350	hypothetical prote
20	86.5	8.7	123	2 B86656	hypothetical prote
21	86	8.6	357	2 A95190	hypothetical prote
22	86	8.6	357	2 B98056	hypothetical prote
23	86	8.6	5627	2 C83339	hypothetical prote
24	85.5	8.6	302	2 S71334	acetyl xylan ester
25	85.5	8.6	382	2 A87548	3-carboxy-cis,cis-
26	85.5	8.6	6486	2 T31076	tyrocidine synchet
27	84.5	8.5	2082	2 T37056	probable multi-dom
28	84.5	8.5	4848	2 T30289	pristinamycin I sy
29	83.5	8.4	338	2 A83846	stage V sporulatio

30	83.5	8.4	665	2 F97032	beta-glucosidase f
31	83	8.3	329	2 B46678	endoglucosidase F3
32	82.5	8.3	398	2 D83214	conserved hypothet
33	82	8.2	619	2 H84416	hypothetical prote
34	81.5	8.2	317	2 B82637	bifunctional bioti
35	81.5	8.2	453	2 H81308	Glu-trNAGln amidot
36	81	8.1	202	2 D71005	hypothetical prote
37	81	8.1	380	2 B70544	probable histidino
38	81	8.1	592	1 S13391	endo-1,4-beta-xyla
39	80.5	8.1	506	2 B72396	sugar kinase, FGYA
40	79.5	8.0	200	2 A69903	hypothetical prote
41	79.5	8.0	342	2 A97184	stage V sporulatio
42	79.5	8.0	749	2 E95889	probable dehydroge
43	79.5	8.0	1075	2 T48805	hypothetical prote
44	79	7.9	322	2 AH3011	thioredoxin trxA l
45	79	7.9	331	2 G98272	probable thioredox

ALIGNMENTS

RESULT 1

S20448
cutinase (EC 3.1.-) - rice blast fungus
C:Species: Magnaporthe grisea (rice blast fungus)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S20448
R:Sweigard, J.A.; Chumley, F.G.; Valent, B.
Mol. Gen. Genet. 232, 174-182, 1992
A>Title: Cloning and analysis of CUT1, a cutinase gene from Magnaporthe grisea.
A:Reference number: S20448; MUID:92212279; PMID:1557023
A:Accession: S20448
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-228 <SWE>
A:Cross-references: UNIPROT:P30272; UNIPARC:UPI000012871C; GB:X61500; NID:G2928; PIDN:CA

Query Match

Best Local Similarity 59.6%; Score 593.5; DB 1; Length 228;
Matches 116; Conservative 27; Mismatches 51; Indels 1; Gaps 1;
Qy 1 QLGAIENGLESGSANACPDAILIFARGSTEPQNGITVGPALANGLESHIRN-INTQGVG 59
Db 33 QLSNVRNDLISGNAACPSVILIIFARASGEVGNMGLSAGTNVASRLERFRNDIWWQGVG 92
Qy 60 GPYDAALATNPLPRGTSQANIDEGKRLFPALANQKCPNTPVVAGYSQGAALIAAAVSELS 119
Db 93 DPYDAALSPNPLPAGTTQGAIDEAKRMFTLANTKCPNAAVAVAGYSQGTAVMFNAVSEMP 152
Qy 120 GAVKEQKGVAFGYTONLQNRGIANVPRRTKVFQNVGAVCTGTLLITPAHLSYTTT 179
Db 153 AAVODQIKGVVLFYGTKNLQNRGIPDPPTKTEVYCNASDAVCFGLTLLPAHFLYTTT 212
Qy 180 ARGEAARFLDRIRA 194
Db 213 SSIAAPNWLIRQIRA 227

RESULT 2

B27451
cutinase (EC 3.1.-) precursor - anthracnose fungus (Colletotrichum gloeosporioides)
C:Species: Glomerella cingulata, Colletotrichum gloeosporioides
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: B27451
R:Ettinger, W.F.; Thukral, S.K.; Kolattukudy, P.E.
Biochemistry 26, 7883-7892, 1987
A>Title: Structure of cutinase gene, cDNA, and the derived amino acid sequence from phyto
A:Reference number: A90524
A:Accession: B27451

```
A:Molecule type: DNA
A:Residues: 1-224 <ETT>
A:Cross-references: UNIPROT:P11373; UNIPARC:UPI000012871A
C:Comment: The cleavage site for the signal peptide is unknown.
C:Genetics:
A:Introns: 63/3
A:Superfamily: cutinase
C:Keywords: hydrolase
F:46-194,125-187/Disulfide bonds: #status predicted
F:96,136,204/Active site: Asp, Ser, His #status predicted

Query Match 57.8%; Score 576; DB 2; Length 224;
Best Local Similarity 58.5%; Pred. No. 1.5e-44;
Matches 110; Conservative 28; Mismatches 48; Indels 2; Gaps 1;

QY 7 NGLSGSANACPDAILIFARGSTPGNMGITVGPALANGLES--HIRNIWIOGVGGPYDA 64
Db 36 NELETGSSSACPKVIYIFARASTEPGNGMISAGPIVADALERIYGANNVWVQVGGPYLA 95

QY 65 ALATNPLPGTSGQANIDEGKRLFALANOKCPNTPVAVGGYSQGAALIAAAVSELGAVKE 124
Db 96 DLASNFLPDGTSSAALNEARLFTLANTRKCPNAAIVSGGYSQGTAVWAGSISGLSTIKN 155

QY 125 QVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGLTIITPAHLSTYIEARGE 184
Db 156 QIKGVVLFYGTQNLQNLGRIPNPFSTKTEYVCALADAVCVGTLFILPAHFLYQDAATA 215

QY 185 ARFLRDRI 192
Db 216 APEFLQARI 223

RESULT 3
S21427
cutinase - fungus (Ascochyta rabiei)
C:Species: Ascochyta rabiei
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S21427
R:Tenhaken, R.; Barz, W.
submitted to the EMBL Data Library, April 1992
A:Description: Characterization and cloning of cutinase from Ascochyta rabiei.
A:Reference number: S21427
A:Accession: S21427
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-223 <TEN>
A:Cross-references: UNIPROT:P29292; UNIPARC:UPI0000128716; EMBL:X65628; NID:g2472; PIDN:
C:Genetics:
A:Introns: 63/3
C:Superfamily: cutinase

Query Match 56.6%; Score 564; DB 1; Length 223;
Best Local Similarity 58.8%; Pred. No. 1.8e-43;
Matches 112; Conservative 29; Mismatches 48; Indels 2; Gaps 2;

QY 5 IENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLES--IRNIWIOGVGGPYD 63
Db 34 ISELEQSSSSCPKAILIFARGSTIENGWGSAGFAVASALRAYGADQIIVWGVGGPYT 93

QY 64 ALATNPLPGTSGQANIDEGKRLFALANOKCPNTPVAVGGYSQGAALIAAAVSELGAVK 123
Db 94 ADLPNPLPGTSGQANINEAVRLFNEANTKCPSTPIVAGGYSQGTAVWAGAIKPLD-AVR 152

QY 124 EQKGVVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGLTIITPAHLSTYIEARGE 183
Db 153 ARVVGTVLFGYTONQNNKGIKDYPQEDLQVYCEVGDVCDGTLTIITVSHFLYLEAAGP 212

QY 184 ARFLRDRI 194
Db 213 APEFLSKIGA 223

RESULT 4
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A27451
cutinase (EC 3.1.1.-) precursor - anthracnose fungus (Colletotrichum capsici) (fragments
C:Species: Colletotrichum capsici
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A27451
R:Bttinger, W.F.; Thukral, S.K.; Kolattukudy, P.E.
Biochemistry 26, 7883-7892, 1987
A:Title: Structure of cutinase gene, cDNA, and the derived amino acid sequence from phyto
A:Reference number: A90524
A:Accession: A27451
A:Molecule type: DNA
A:Residues: 1-228 <ETT>
A:Cross-references: UNIPROT:P10951; UNIPARC:UPI0000128719
C:Comment: The cleavage site for the signal sequence is not known.
C:Genetics:
A:Introns: 66/3
C:Superfamily: cutinase
C:Keywords: hydrolase
F:49-198,129-191/Disulfide bonds: #status predicted
F:99,140,208/Active site: Asp, Ser, His #status predicted

Query Match 55.3%; Score 550.5; DB 2; Length 228;
Best Local Similarity 57.1%; Pred. No. 3e-42;
Matches 108; Conservative 27; Mismatches 51; Indels 3; Gaps 2;

QY 7 NGLSGSANACPDAILIFARGSTPGNMGITVGPALANGLES--IRNIWIOGVGGPYDA 64
Db 39 NELESGSSSNCPKVIYIFARASTEPGNGMISAGPIVADALESRYGASQVWVQVGGPYSA 98

QY 65 ALATNPLPGTSGQANIDEGKRLFALANOKCPNTPVAVGGYSQGAALIAAAVSELGAVK 123
Db 99 DLASNFLPDGTSGKRVINEAKRLFTLANTRKCPNAAIVSGGYSQGTAVWAGSISGLSTIQ 158

QY 124 EQKGVVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGLTIITPAHLSTYIEARGE 183
Db 159 NQIKGVVLSAITKMLQNLGRIPNPFSTKTEYVCALADAVCVGTLFILPAHFLYQADAATS 218

QY 184 ARFLRDRI 192
Db 219 APEFLAARI 227

RESULT 5
UVFUS
cutinase (EC 3.1.1.-) precursor - fungus (Fusarium solani)
C:Species: Fusarium solani f.sp. pisi
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A32836; A00731, B00731; A61421
R:Soliday, C.L.; Dickman, M.B.; Kolattukudy, P.E.
J. Bacteriol. 171, 1942-1951, 1989
A:Title: Structure of the cutinase gene and detection of promoter activity in the 5'-fla
A:Reference number: A32836; MUID:89197761; PMID:2703464
A:Accession: A32836
A:Molecule type: DNA
A:Residues: 1-47, 'A', 49-93, 'A', 95-230 <SOL>
A:Cross-references: UNIPROT:P00590; UNIPARC:UPI00001688FB; GB:M29759; NID:g168147; PIDN:
A:Note: the authors translated the codon GCA for residue 94 as Arg
R:Soliday, C.L.; Flurkey, W.H.; Okita, T.W.; Kolattukudy, P.E.
Proc. Natl. Acad. Sci. U.S.A. 81, 3939-3943, 1984
A:Title: Cloning and structure determination of cDNA for cutinase, an enzyme involved in
A:Reference number: A00731
A:Accession: A00731
A:Molecule type: mRNA
A:Residues: 1-230 <S02>
A:Cross-references: UNIPARC:UPI0000128702; GB:K02640; NID:g168145; PIDN:AAA33334.1; PID:
A:Accession: B00731
A:Molecule type: protein
A:Residues: 57-94,113-142,183-192 <S03>
A:Cross-references: UNIPARC:UPI0000172739; UNIPARC:UPI000017273A; UNIPARC:UPI000017273B
R:Soliday, C.L.; Kolattukudy, P.E.
Biochem. Biophys. Res. Commun. 114, 1017-1022, 1983
A:Title: Primary structure of the active site region of fungal cutinase, an enzyme invol
A:Reference number: A61421; MUID:83308716; PMID:6412706
```

A:Accession: A61421
A:Molecule type: protein
A:Residues: 113-142 <S04>
A:Cross-references: UNIPARC:UPI000017273A
R:Lin, T.S.; Kolattukudy, P.E.
Eur. J. Biochem. 106, 341-351, 1980
A:Title: Structural studies on cutinase, a glycoprotein containing novel amino acids and
A:Reference number: A44665; MUID:90245930; PMID:7398618
A:Contents: annotation; identification of glucuronylated amino end
C:Comment: This enzyme catalyzes the hydrolysis of cutin, a polyester that forms the str
C:Comment: Southern blot results suggest that the genome contains two copies of the cuti
C:Genetics: 64/3
A:introns: 64/3
C:Superfamily: cutinase
C:Keywords: blocked amino end; glycoprotein; hydrolase
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-230/Product: cutinase #status predicted <MAT>
F:32/Modified site: glucuronylated amino end (Gly) (in mature form) #status experimental
F:125-187/Disulfide bonds: #status experimental
F:136,204/Active site: Ser, His #status experimental

Query Match 54.7%; Score 545; DB 1; Length 230;
Best Local Similarity 54.8%; Pred. No. 9.5e-42;
Matches 108; Conservative 32; Mismatches 53; Indels 4; Gaps 3;

Qy 1 QLG-ATENGLEGSANACPDAILIFARGSTPEPNNGITVGPALANGLESHT--RNIIQIG 57
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 30 QLGRITRDDLLINGNSASCRDVIYFARGSTETNGLG-TLGPISIANLESFAFGKGVWQIG 88
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Qy 58 VGGPYDAALATNPLPGTQOANTIDEGKRLPALANQKCPNTPVAGGYSGQAALIAAVSE 117
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 89 VGGAYRATLGDNALPRTGTSAAIREMLGLFQOATKCPDATLIAGGYSGQAALAAASIT 148
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Qy 118 LSGAVKEQVKVALFCVTQNLQNRGGIANYPRETKVFCNVGDAVCTGLITPAHLSVT 177
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 149 LOSAIRDKIAGTVLFGYTKNLQNRGRIPNYPADRTKFCNTGDLVCTGSLIVAAPHLAYG 208
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Qy 178 IEARGEAAARFLDRIRA 194
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 209 PDARGPAPEFLIEKVRA 225
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

RESULT 6
F70756
probable cutinase precursor with N-terminal signal sequence - Mycobacterium tuberculosis
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70756
R:Colle, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, K.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70756
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-217 <COL>
A:Cross-references: UNIPROT:Q10837; UNIPARC:UPI000003181B; GB:Z74025; GB:AL123456; NID:9
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv1984C
C:Superfamily: cutinase

Query Match 19.0%; Score 189.5; DB 2; Length 217;
Best Local Similarity 30.8%; Pred. No. 1e-09;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

Qy 8 GLESGANACPDAILIFARGSTPEPNNGITVGPALANGLESHTRNIIQVGGPYDAALA 67
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 26 GGRAAHADPCSDIAVVFARGTTHQASGLIG-DVGEAFVDSLTSQ-----VGGRSIGVYA 76
||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

[illegible]

E70796
Probable cutinase precursor - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: E70796
; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: E70796
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-187 <COL>
A:Cross-references: UNIPARC:UPI000016537B; GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CA
A:Experimental source: strain H37RV
C:Genetics:
C:Gene: RV3724
C:Superfamily: cutinase

	Query Match	11.6%;	Score 115.5;	DB 2;	Length 187;
	Best Local Similarity	27.6%;	Pred. No. 0.0039;		
	Matches	45;	Conservative 22;	Mismatches 73;	Indels 23; Gaps 7;

Qy 51 RNWITQGGVGYDAALATNFLPRGTSQANIDEGKRLFALANQKPNTPVAGYSQGAAL 110
::: | ::| :
Db 27 KSLGVYAVNYPASNDPFASSDFPKTVTGIRDAGSHIQSMA-MSCPQTRQLVGYSQGAIV 85
::: | ::| :
Qy 111 -----TAAVSSELSGAKVEQVKGVALFG--YTQNLIQRGG--IANYP--RE 150
::: | ::| :
Db 86 AGYVTSAVVPAPVPOAVPAPEVANHVAAVTLEGPASQAFLGQYGAPPPIATIGLYQP 145
::: | ::| :
Qy 151 RTKVFCNVGDVACTGLTIITPAHLSYTIEAR-GEAARFLRDRI 192
::: | ::| :
Db 146 KTLQCADGDSIC-DGNSPVAHLGYAVNGMWGGANFAASRL 187
::: | ::| :

RESULT 11
G70987
Probable cutinase - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: G70987
; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70987
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-174 <COL>
A:Cross-references: UNIPARC:UPI00000D5B96; GB:Z95890; GB:AL123456; NID:g3242245; PIDN:CA
A:Experimental source: strain H37RV
C:Genetics:
C:Gene: RV1758
C:Superfamily: cutinase

```

DB      77  LQHHGGDGAN-DAISHIKIMAS-SCPNTKLVLLGGYSQGATVDDIVAGVPLGSLSFSGSLP 134
QY      120 GAVKEOVKGVALPYQNTLQNRGG-----IANYPRERTKVFQNVGDAVCTGTGLTIIPAH 174
DB      135 AAYADNVAAVAVFG-----NPSNRAGGSLSLSPFGSKAIDLCNPTDPIC-----HV 182
QY      175 SYTIEARG-----EAARFLDRDRA 194
DB      183 GPGNEFSCHIDGYIPYTTTQAASFVVQRLRA 213

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RESULT 10

	Query Match	9.8%;	Score 98;	DB 2;	Length 174;
	Best Local Similarity	29.9%;	Pred. NO.	0.14;	
	Matches	52;	Conservative	22;	Mismatches 64; Indels 36; Gaps 12;
Qy	44 NGLSESHI--RNIIWIGVGGPYDAALATNLFPRGTSOANI-DEGRKLPFALANOKCENTPVV	100	:	:	: :
Dd	11 DALRSKIKEKSNGYGVDP-----ATTDFP-TAMAGIYDAGTHVEQTQA-ANCPSQSILV	62	:	:	: :
Qy	101 AGGYISQGAAHI-----AAAASE-----LSCAVKEOVKGVALFGY--TQNLRNGG--	143	:	:	: :
Dd	63 LGGFSGGAARVMGFVTAAAIIDPGAPLDADRPMPPEVAHDHVAANTFLGMSPSVAFMHSIGAPP	122	:	:	: :

RESULT 10

Qy 144 --TANYPRETKVCNVDAVCT--GTLITPAHLSTYIEARG-AAFLFLDRI 192
Db 123 IVIGPLYAEKTIQICAPGDPVCSGGN---WAAHNGYADGMVQNAVFAAGRL 173

RESULT 12
F70887
hypothetical protein Rv3802c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: F70887
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: F70887
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-336 <COL>
A:Cross-references: UNIPROT:O53581; UNIPARC:UPI00000D11D1; GB:AL022076; GB:AL123456; NID
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3802c

Query Match 9.6%; Score 96; DB 2; Length 336;
Best Local Similarity 22.4%; Pred. No. 0.46;
Matches 50; Conservative 24; Mismatches 83; Indels 66; Gaps 10;

Qy 16 ACPDAILIFARGSTE-----PGNMGITV-GPALANGLESHIRNIWQGVGGP 61
Db 71 SCDFQVMISVPGTWESPQONPLNPVQFPKALLKVTGTAQAPARVQTYTVAQF 130

Qy 62 YDAALATNLFPRGTSQANIDEGKRLFALA----NQKCPNTPVAGVSGQAALIAAVSE 117
Db 131 HNPLTTDNQMSYNDRA---EGTRAMVAAMTMNRCPLTSYVLIGFSQGAIVAGDVASD 187

Qy 118 LS---GAVKEQ-VKGVAFGYTQNLQNRGGIANY----- 147
Db 188 IGNRGPRVDLDVLGVTLIADGRQ---GVGNQVPPSPRGEABITLHEVPVLSGLGLT 244

Qy 148 ---PRE-----RTKVCNVGDVACTG-TLITPAHLSVTI 178
Db 245 MTGPRPGGFGALDGRINEICAQGLICAPAAQAFSPANLPTTL 287

RESULT 13
T35575
hypothetical protein SC6G4.24 SC6G4.24 - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35575
R:Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21583
A:Accession: T35575
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-420 <SAU>
A:Cross-references: UNIPROT:O86787; UNIPARC:UPI00000DAD79; EMBL:AL031317; PIDN:CAA20402
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC6G4.24

Query Match 9.0%; Score 89.5; DB 2; Length 420;
Best Local Similarity 26.4%; Pred. No. 2.3;
Matches 39; Conservative 22; Mismatches 70; Indels 17; Gaps 6;

Qy 10 EGSANACPDAILIFARGSPGNGMITVGPALAN-----GLSHIRNI-WIQGVGG 60

Db 105 EAG-ADPAPRRRLFRKAPAPVTVVFSHGVCINQDSWHFORAALRGVVRSVYWDQSHG 163
Qy 61 PYDAALATNLFPRGTSQANIDB-GKRLPALANQKCPNTPVAGVSGQAALIAAAVSELS 119
Db 164 RSGRGVAQT---RDDRVPVSIIEGLRDLKAVIDAAAPEGPIVLVGHSMGGMTVMALADAFP 220

Qy 120 GAVKEQVKGVAFGYTQNLQNRGGIANY 147
Db 221 DLVRRVVGVVALVGTS---SGRLGEVNF 245

RESULT 14
R85557
enterobactin synthetase component EntF [similarity] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: R85557
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: R85557
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1293 <STO>
A:Cross-references: UNIPROT:Q8XBV9; UNIPARC:UPI0000129FD3; GB:AE005174; NID:G12513476; E
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: entF
C:Superfamily: enterobactin synthetase component F; acetate-CoA ligase homology; acyl
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F;1006/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 8.8%; Score 88; DB 2; Length 1293;
Best Local Similarity 24.7%; Pred. No. 12;
Matches 57; Conservative 26; Mismatches 84; Indels 64; Gaps 13;

Qy 1 QLGAIENGLESGSANACPDAILIFARGSTPCNGMITVGPAL-----ANG-----LBS 48
Db 1037 KLATIIDGEEDSSRRMGFETILPLREGN-----GPTLFCFHPASGFAPQFVLSR 1086

Qy 49 HIRNIW-IQGVGYPYDAALATNLFPRGTSQ---ANIDE--GKRLFALANQKCPNTPVAGG 103
Db 1087 YLDPLMSLIQISP-----RPHGPMQTALNDEVCEHAHLATLLEQQ-PHGYPYLLG 1136

Qy 104 YSQAALIAAAVSELGSAVKQVKGVAFG-----YTONLQNRGG-----TANYPRER- 151
Db 1137 YSLGTTLAQGIARLR-ARGEQVAFGLDTPPETONWQKEANGLDPEVLAEINRERE 1195

Qy 152 -----TKVFCNVGDVACTGTLITPAHLSVTIEARGEAAARFLDRD 191
Db 1196 AFLAAQGSSTELFTTIEGYNADVRLTLTAH---SVFPDGKATLFAER 1243

RESULT 15
A90707
enterobactin synthetase component EntF [imported] - Escherichia coli (strain O157:H7, su
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: A90707
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A90707
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1293 <HAY>
A:Cross-references: UNIPROT:Q8XBV9; UNIPARC:UPI0000129FD3; GB:BA000007; PIDN:BA334048.1;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:

A:Gene: ECs0625
C:Superfamily: enterobactin synthetase component F; acetate-CoA ligase homology; acyl ca
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:1006/Binding site: phosphopantetheine (Ser) (covalent) #status predicted

Query Match 8.8%; Score 88; DB 2; Length 1293;
Best Local Similarity 24.7%; Pred. No. 12;
Matches 57; Conservative 26; Mismatches 84; Indels 64; Gaps 13;

QY 1 QLGAIEENGLESANACPDAILIFARGSTPEGNMGITVGPAL-----ANG-----LES 48
Db 1037 KLATIIDGEEDSRRMGFETILPLREGN-----GPTLCFHPASGFANQFSVLSR 1086
QY 49 HIRNIW-IOGVGYPYDAALATNPLPRGTSQ--ANIDE--GKRLFALANQKCPNTPVVAGG 103
Db 1087 YLDPLWSIIIGIQSF-----RPHGPMQTATNLDEVCEAHLATLLEQQ-PHGPYYLLG 1136
QY 104 YSGAALIAAAVSELSGAVKEQVKGVALFG-----YTQNLQNRGG-----IANYPRER- 151
Db 1137 YSLGGTLAQGIARLR-ARGEQVAFGLGLLTWPPETQNWQKEANGLDPEVLAEINRERE 1195
QY 152 -----TKVFCNVGDVCTGTLLITPAHLSVTIEARGHAARFLDR 191
Db 1196 AFLAAQGGSTSELTFTIEGNYADAVRLITAH---SVPFDGKATLFVAER 1243

Search completed: February 4, 2006, 04:57:00
Job time : 46 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:48:38 ; Search time 253 Seconds

(without alignments)
540.998 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESANACPD.....SYTIARGEARFLRDIRA 194

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	596	59.8	209	1 CUTI_ALTPR	P41744 alternaria
2	595.5	59.8	228	2 Q52AU1_MAGGR	Q52au1 magnaporthe
3	593.5	59.6	228	1 CUTI_MAGGR	P30272 magnaporthe
4	576	57.8	224	1 CUTI_COLGL	P11373 colletotric
5	576	57.8	227	2 Q41I88_GIBZE	Q41i88 gibberella
6	575	57.7	248	2 Q41KB6_GIBZE	Q41kb6 gibberella
7	564	56.6	223	1 CUTI_ASCRA	P29292 ascochyta r
8	550.5	55.3	228	1 CUTI_COLCA	P10951 colletotric
9	550	55.2	230	1 CUTI_FUSSC	Q99174 fusarium so
10	545	54.7	230	1 CUTI1_FUSSO	P00590 fusarium so
11	543.5	54.6	231	2 Q41H51_GIBZE	Q41h51 gibberella
12	542.5	54.5	231	1 CUTI2_FUSSO	Q96ut0 fusarium so
13	540.5	54.3	231	1 CUTI3_FUSSO	Q96u89 fusarium so
14	494	49.6	217	2 Q4W924_ASPFU	Q4w924 aspergillus
15	467.5	46.9	214	2 Q4WQ24_ASPFU	Q4wq24 aspergillus
16	465.5	46.7	213	2 Q5B2C1_EMENI	Q5b2c1 aspergillus
17	463.5	46.5	221	2 Q5AX00_EMENI	Q5ax00 aspergillus
18	458	46.0	211	2 Q4X1N0_ASPFU	Q4x1n0 aspergillus
19	450	45.2	213	1 CUTI_ASPOR	P52956 aspergillus
20	444	44.6	257	2 Q5AV79_EMENI	Q5av79 aspergillus
21	412.5	41.4	228	2 Q51N02_MAGGR	Q51n02 magnaporthe
22	329	33.0	214	2 Q51KM8_MAGGR	Q51km8 magnaporthe
23	311	31.2	230	2 Q4HWM4_GIBZE	Q4hwm4 gibberella
24	269	27.0	427	2 Q4IM18_GIBZE	Q4im18 gibberella
25	262	26.3	254	2 Q9P960_ASPOR	Q9p960 aspergillus
26	242.5	24.3	686	2 Q5B9E7_EMENI	Q5b9e7 aspergillus
27	241.5	24.2	375	2 Q4X078_ASPFU	Q4x078 aspergillus
28	240.5	24.1	216	2 Q52018_MAGGR	Q52018 magnaporthe
29	236	23.7	234	2 Q529T3_MAGGR	Q529t3 magnaporthe
30	234.5	23.5	1003	2 Q51V73_MAGGR	Q51v73 magnaporthe
31	229.5	23.0	201	1 CUTI_MONFR	Q8tgb8 monilinia f

32	228	22.9	202	1 CUTI_BOTCI	Q00298 botrytis ci
33	222.5	22.3	203	1 CUTI_PYBR	Q9Y7g8 pyrenopeziz
34	220	22.1	190	2 Q51H99_MAGGR	Q51h99 magnaporthe
35	206.5	20.7	287	2 Q529U1_MAGGR	Q529j1 magnaporthe
36	205.5	20.6	236	1 CUTI_ERYGR	Q8xlp1 erysiphe gr
37	195	19.6	217	2 Q58G92_PHYIN	Q58g92 phytophthor
38	193	19.4	211	2 Q73S40_MYCPA	Q73s40 mycobacteri
39	189.5	19.0	217	1 CUT1_MYCBO	P63880 mycobacteri
40	189.5	19.0	217	1 CUT1_MYCTU	P63879 mycobacteri
41	186.5	18.9	230	1 CUT2_MYCBO	P63882 mycobacteri
42	186.5	18.9	230	1 CUT2_MYCTU	P63881 mycobacteri
43	187.5	18.8	639	2 Q4P198_USTMA	Q4p198 ustilago ma
44	182	18.3	234	2 Q73ZX5_MYCPA	Q73zx5 mycobacteri
45	181.5	18.2	235	2 Q73UB0_MYCPA	Q73ue0 mycobacteri

ALIGNMENTS

RESULT 1

ID	CUTI_ALTPR	STANDARD;	PRT;	209 AA.
AC	P41744;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	10-MAY-2005 (Rel. 47, Last annotation update)			
DE	Cutinase precursor (BC 3.1.1.74) (Cutin hydrolase).			
OS	Name=CUTAB1;			
OS	Alternaria brassicicola.			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;			
OC	Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.			
OK	NCHI_TaxID=29001;			
RP	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Yao C., Koeller W.;			
RL	Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that			
CC	penetrates through the cuticular barrier into the host plant during			
CC	the initial stage of the fungal infection (By similarity).			
CC	-1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- SIMILARITY: Belongs to the cutinase family.			
CC	-----			
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use as long as its content is in no way modified and this statement is not			
CC	removed.			
CC	-----			
CC	EMBL; U03393; AAA03470.1; -; Unassigned_RNA.			
DR	HSSP; P00590; 1XZG.			
DR	InterPro; IPR000675; Cutinase.			
DR	InterPro; IPR01150; Cutinase_monf.			
DR	Pfam; PF01083; Cutinase; 1.			
DR	PIRSF; PIRSF000861; Cutinase; 1.			
DR	PRINTS; PR00129; CUTINASE.			
DR	PROSITE; PS00155; CUTINASE_1; 1.			
DR	PROSITE; PS00933; CUTINASE_2; 1.			
DR	Hydrolase; Serine esterase; Signal.			
KW	SIGNAL 1 ? Potential.			
FT	CHAIN 1 ?			
FT	ACT_SITE 119 119			
FT	ACT_SITE 174 174			
FT	ACT_SITE 187 187			
FT	DISULFID 29 177			
FT	DISULFID 108 170			
FT	SEQUENCE 209 AA; 21649 MW; 1756D06D84093A64 CRC64;			

Query Match 59.8%; Score 596; DB 1; Length 209;

Best Local Similarity 60.3%; Pred. No. 5.1e-43;

Matches 117; Conservative 22; Mismatches 53; Indels 2; Gaps 1;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLES--HINNIWQGV 58
 Db 13 QASTTRNELETGSSDACPRTIFIFARGSTPGNMGALVGPFTANALAESAYGNVWVQGV 72
 QY 59 GGPYDAALATNPLPRTGTSOANIDEGKRLPALANOKCPNTPVAVAGGYSQGAALIAAAVSEL 118
 Db 73 GGPYTAGLVENALPAGTSQAIREAORLFWLAAKCPNTPITAGGYSQGANVMSNAIPGL 132
 QY 119 SGAVKEQVKGVALFGYTONLQNRGGIANYPRTKVCNVDGAVCTGTLLITPAHLISYTI 178
 Db 133 SAAVQDQIKGVVLFYGTKNLQNGRIPNPTSTKTIYCVETGDLVCGTLLITPAHLISYD 192
 QY 179 EARGEAAARFLDRRI 192
 Db 193 EAAVQAPTFLRAQI 206

RESULT 2
 Q52AUI MAGGR PRELIMINARY; PRT; 228 AA.
 AC Q52AUI;
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MG01943.4;
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachi H., Ambuster J., Bachansang P., Baldwin J., Barry A.,
 RA Bayl T., Blitshstein B., Bloom T., Biye J., Boguslavskiy L.,
 RA Borowsky M., Bougualter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hogopian D., Higos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Huby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseles M., Karlsson B.,
 RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
 RA Manning J., Marbella R., Maru K., Matthews C., Mauceli E.,
 RA McCarthy M., McDonough S., McGhee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelson T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotsho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Plunkhug P., Piquani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stenson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
 RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
 RA Towey S., Taamia T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RT "The genome sequence of Magnaporthe grisea."
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AACU01000378; EAA53958.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 228 AA; 24191 MW; 36BF2F253B8F7709 CRC64;

Query Match 59.8%; Score 595.5; DB 2; Length 228;
 Best Local Similarity 59.5%; Pred. No. 6.2e-43;
 Matches 116; Conservative 27; Mismatches 51; Indels 1; Gaps 1;

QY 1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLES--HINNIWQGV 59
 Db 33 QLNSVRNDLISGNAACPSVILLIFARASGEVGNMGLSAGTNVASALEREFRNDIWWQGVG 92
 QY 60 GPYDAALATNPLPRTGTSOANIDEGKRLPALANOKCPNTPVAVAGGYSQGAALIAAAVSEL 119
 Db 93 DPYDAALSPNPLPAGTTQGAIDEAKRMFTLANTKCPNAAVAVAGGYSQGTAVMFAVSEMP 152
 QY 120 GAVKEQVKGVALFGYTONLQNRGGIANYPRTKVCNVDGAVCTGTLLITPAHLISYTI 179
 Db 153 AAVQDQIKGVVLFYGTKNLQNGRIPDPTKTEIVICNASDAVCFGLFLPAHLISYTI 212
 QY 180 ARGEAAARFLDRIR 194
 Db 213 SSIAAPNWLIRQIRA 227

RESULT 3
 ID CUTI_MAGGR STANDARD; PRT; 228 AA.
 AC P30272;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
 GN Name=CUTI;
 OS Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=148305;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=4091-S-8;
 RC MEDLINE=92212279; PubMed=1557023;
 RX Sweigard J.A., Chumley F., Valent B.;
 RA "Cloning and analysis of CUT1, a cutinase gene from Magnaporthe
 grisea";
 RT Mol. Gen. Genet. 232:174-182(1992).
 RL -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
 forms the structure of plant cuticle. Allows pathogenic fungi to
 penetrate through the cuticular barrier into the host plant during
 the initial stage of the fungal infection.
 CC -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the cutinase family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

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DR EMBL; X61500; CAA43717.1; ALT_TERM; Genomic_DNA.
DR PIR; S20448; S20448.
DR HSSP; P00590; 1CUW.
DR InterPro; IPR000675; Cutinase.
DR InterPro; IPR011150; Cutinase_monf.
DR Pfam; PF01083; Cutinase; 1.
DR PIRSF; PIRSF000861; Cutinase; 1.
DR PRINTS; PR00129; CUTINASE.
DR PROSITE; PS00155; CUTINASE_1; 1.
DR PROSITE; PS00931; CUTINASE_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 228 Cutinase.
FT ACT_SITE 138 138 By similarity.
FT ACT_SITE 193 193 By similarity.
FT ACT_SITE 206 206 By similarity.
FT CARBOHYD 190 190 N-linked (GlcNAc...) (Potential).
FT DISULFID 49 196 By similarity.
FT DISULFID 127 189 By similarity.
SQ SEQUENCE 228 AA; 24277 MW; BB0ACE063B9D4627 CRC64;

Query Match 59.6%; Score 593.5; DB 1; Length 228;
Best Local Similarity 59.5%; Pred. No. 9.1e-43;
Matches 116; Conservative 27; Mismatches 51; Indels 1; Gaps 1;

QY 1 QLGATENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRN-INTQGVG 59
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33 QLSVRNDLISGNAACPSVILIFARASGEVGNMGLSAGTNVASRLERFRNDIIVQGVG 92
QY 60 GPYDAALATNPLPGTSGQANIDEGKLFALANOKCPTVPVAGGYSQGAALIAAVALS 119
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
93 DYPDALSPNPLPAGTQTGAIDKRMFTLANTKCPNAAVAVAGGYSQGTAVMFPVSEMP 152
QY 120 GAVKEQVKALVFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLTITPAHLGYTIE 179
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
153 AAVQDIKGVLFGYTKNLQNLGRIPNFTSKTEVYCDIADAVCYGTLFLPAHFLYQTDAAVA 212
QY 180 ARGEAARFLDRIRA 194
Db :|||:|||||:
213 SSIAAPNWLIRQIRA 227

RESULT 4
CUTI_COLGL STANDARD; PRT; 224 AA.
AC P11373; O8X1A3;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cutinase precursor (BC 3.1.1.74) (Cutin hydrolase).
GN Name=CUTA;
OS Colletotrichum gloeosporioides (Anthracnose fungus) (Glomerella cingulata).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Glomerella.
OX NCBI_TaxID=5457;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ettinger W.F., Thukral S.K., Kolatukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid sequence from phytopathogenic fungi.";
RL Biochemistry 26:7883-7892(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Abu Bakar F.D., Cooper D.M., Zamrod Z., Mahadi N.M., Sullivan P.A.;
RT "Cloning and characterization of the cutinase-encoding gene and cDNA from the fungal phytopathogen, Glomerella cingulata.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that forms the structure of plant cuticle. Allows pathogenic fungi to penetrate through the cuticular barrier into the host plant during the initial stage of the fungal infection.

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CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By contact with cutin.
CC -!- PTM: The 2 disulfide bonds play a critical role in holding the catalytic residues in juxta-position; reduction of the disulfide bridges results in the complete inactivation of the enzyme.
CC -!- SIMILARITY: Belongs to the cutinase family.
CC -----
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CC -----
CC EMBL; M21443; AAA33042.1; -; Genomic DNA.
CC EMBL; AF444194; AAL38030.1; -; Genomic DNA.
CC PIR; B27451; B27451.
CC HSSP; P00590; 1CUW.
CC InterPro; IPR000675; Cutinase.
CC InterPro; IPR011150; Cutinase_monf.
CC Pfam; PF01083; Cutinase; 1.
CC PIRSF; PIRSF000861; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
KW Hydrolase; Serine esterase; Signal.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 224 Cutinase.
FT ACT_SITE 136 136 By similarity.
FT ACT_SITE 191 191 By similarity.
FT ACT_SITE 204 204 By similarity.
FT DISULFID 46 194 By similarity.
FT DISULFID 125 187 By similarity.
FT CONFLICT 6 7 VL -> IV (in Ref. 2).
FT CONFLICT 83 83 N -> D (in Ref. 2).
SQ SEQUENCE 224 AA; 23477 MW; IC5BACEAB469ABFA CRC64;

Query Match 57.8%; Score 576; DB 1; Length 224;
Best Local Similarity 58.5%; Pred. No. 2.8e-41;
Matches 110; Conservative 28; Mismatches 48; Indels 2; Gaps 1;

QY 7 NLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLES--HIRNIWQGVGPPYDA 64
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
36 NELETGSSACPKVIYIFARASTPEGNMGISAGIVADALERIYGANNVVGQGVGPVLA 95
QY 65 ALATNPLPGTSGQANIDEGKLFALANOKCPTVPVAGGYSQGAALIAAVALSGLAVKE 124
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 DLASNPLPDGTSSAAINEARRLFTLANTKCPNAAIVSGGYSQGTAVMAGSISGLSTTIKN 155
QY 125 QVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVCTGTLTITPAHLSYTIARGEA 184
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
156 QIKGVVLFGYTKNLQNLGRIPNFTSKTEVYCDIADAVCYGTLFLPAHFLYQTDAAVA 215
QY 185 ARFLDRIR 192
Db |||:|||||:
216 PRELQARI 223

RESULT 5
Q4IIR8 GIBZE
ID Q4IIR8_GIBZE PRELIMINARY; PRT; 227 AA.
AC Q4IIR8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG02890.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: By contact with cutin.
CC -!- SIMILARITY: Belongs to the cutinase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X65628; CAA46582.1; -; Genomic_DNA.
CC PIR; S21427; S21427.
CC HGSP; P00590; 1CUW.
CC InterPro; IPR000675; Cutinase.
CC InterPro; IPR011150; Cutinase_monf.
CC Pfam; PF01083; Cutinase; 1.
CC PIRSF; PIRSF000861; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC Hydrolyase; Serine esterase; Signal.
CC SIGNAL 1 19 Potential.
CC CHAIN 20 223 Cutinase.
CC ACT_SITE 135 135 By similarity.
CC ACT_SITE 189 189 By similarity.
CC ACT_SITE 202 202 By similarity.
CC DISULFID 46 192 By similarity.
CC DISULFID 124 185 By similarity.
CC SEQUENCE 223 AA; 1882A5ADD1B5E7FB CRC64;

Query Match 56.6%; Score 564; DB 1; Length 223;
Best Local Similarity 58.6%; Pred. No. 3e-40;
Matches 112; Conservative 29; Mismatches 48; Indels 2; Gaps 2;

QY 5 IENGLESGSNACPDAILLIFARGSTPEGNMGITVGPALANGLESH--IRNWIQVGGPYD 63
DB 34 IRSELEQSSSSCPKAILLIFARGSTPEGNMGITVGPALANGLESH--IRNWIQVGGPYT 93

QY 64 AALATNFPRTGTOANIDEKRLPALANOKCPNTFVVGYSQGAALIAAAVSELGAVK 123
DB 94 ADLPNFPRTGTSQASAINAVRLFNEANTKCPSTPIVAGYSQGTAVWAGAI PKLD-AVR 152

QY 124 EQVKGVALFGYTONLQNRGGIANYPRERTKVFNCNVGDAVCTGLTIITPAHLSYTYEARGE 183
DB 153 ARVVGTVLFGYTONQNNKGIKDYQEDLQVYCEVGLVCDGTLLITVSHFLYLEEAAGP 212

QY 184 AARFLDRIRA 194
DB 213 APEFLKSKIGA 223

RESULT 8
CUTI_COLCA STANDARD; PRT; 228 AA.
AC P10951;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
GN Name=CUTA;
OS Colletotrichum capsici (Anthracnose fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
OC mitosporic Phyllachoraceae; Colletotrichum.
OX NCBI_TaxID=5456;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC STRAIN=ATCC 48574;
RA Eickinger W.F., Thukral S.K., Kolattukudy P.E.;
RT "Structure of cutinase gene, cDNA, and the derived amino acid sequence
RT from phytopathogenic fungi."
RL Biochemistry 26:7883-7892(1987).
CC -!- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that

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CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -!- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By contact with cutin.
CC -!- PTM: The 2 disulfide bonds play a critical role in holding the
CC catalytic residues in juxta-position; reduction of the disulfide
CC bridges results in the complete inactivation of the enzyme.
CC -!- SIMILARITY: Belongs to the cutinase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; M18033; AAA33043.1; -; Genomic_DNA.
CC PIR; A27451; A27451.
CC HGSP; P00590; 1CUW.
CC InterPro; IPR000675; Cutinase.
CC InterPro; IPR011150; Cutinase_monf.
CC Pfam; PF01083; Cutinase; 1.
CC PIRSF; PIRSF000861; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC Direct protein sequencing; Hydrolase; Serine esterase; Signal.
CC SIGNAL 1 16 Potential.
CC CHAIN 17 228 Cutinase.
CC ACT_SITE 140 140 By similarity.
CC ACT_SITE 195 195 By similarity.
CC ACT_SITE 208 208 By similarity.
CC DISULFID 49 198 By similarity.
CC DISULFID 129 191 By similarity.
CC SEQUENCE 228 AA; 23714 MW; 3825D42C23DA139B CRC64;

Query Match 55.3%; Score 550.5; DB 1; Length 228;
Best Local Similarity 57.1%; Pred. No. 4.5e-39;
Matches 108; Conservative 27; Mismatches 51; Indels 3; Gaps 2;

QY 7 NLESGSANCPDAILLIFARGSTPEGNMGITVGPALANGLESH--IRNWIQVGGPYDA 64
DB 39 NELESGSSSCPVIYIFARASTPEGNMGISAGPIVADALESRYGASQVWVQVGGPYSA 98

QY 65 AALATNF-LPRGTSQANIDEKRLPALANOKCPNTFVVGYSQGAALIAAAVSELGAVK 123
DB 99 DLASNFTIPEGTSRVAINAKRLPLTANTKCPNSAVVAGYSQGTAVWASSISLSSTIQ 158

QY 124 EQVKGVALFGYTONLQNRGGIANYPRERTKVFNCNVGDAVCTGLTIITPAHLSYTYEARGE 183
DB 159 NQIKGVVLSAITKNLQNLGRIPNESTKTEVYCALADAVCYGTLFILPAHFLYQADAATS 218

QY 184 AARFLDRIRI 192
DB 219 APRFLAARI 227

RESULT 9
CUTI_FUSSC STANDARD; PRT; 230 AA.
AC Q99174;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cutinase precursor (EC 3.1.1.74) (Cutin hydrolase).
GN Name=CUTA;
OS Fusarium solani subsp. cucurbitae (Nectria ipomoeae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX NCBI_TaxID=57162;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=PCB 153;
RX MEDLINE=97254998; PubMed=9100380;
RA Crowhurst R.N., Binnie S.J., Bowen J.K., Hawthorne B.T., Plummer K.M.,
RD Rees-George J., Rikkersink E.H., Templeton M.D.;
RT "Effect of disruption of a cutinase gene (cutA) on virulence and
RT tissue specificity of Fusarium solani f. sp. cucurbitae race 2 toward
RT Cucurbita maxima and C. moschata.";
RL Mol. Plant Microbe Interact. 10:355-368(1997).
CC -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
CC forms the structure of plant cuticle. Allows pathogenic fungi to
CC penetrate through the cuticular barrier into the host plant during
CC the initial stage of the fungal infection.
CC -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the cutinase family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: U63335; AAB05922.1; -; Genomic_DNA.
CC HSP; P00590; 2CUT.
CC SMR; Q99174; 33-229.
CC InterPro; IPR000675; Cutinase.
CC InterPro; IPR011150; Cutinase_monof.
CC Pfam; PF01083; Cutinase; 1.
CC PIRSF; PIRSF000861; Cutinase; 1.
CC PRINTS; PR00129; CUTINASE.
CC PROSITE; PS00155; CUTINASE_1; 1.
CC PROSITE; PS00931; CUTINASE_2; 1.
CC KW Hydroxylase; Serine esterase; Signal.
CC FT SIGNAL 1 16 By similarity.
CC FT CHAIN 17 230 Cutinase.
CC FT ACT_SITE 136 136 By similarity.
CC FT ACT_SITE 191 191 By similarity.
CC FT ACT_SITE 204 204 By similarity.
CC FT DISULFID 47 194 By similarity.
CC FT DISULFID 125 187 By similarity.
CC SEQUENCE 230 AA; 23902 MW; 05FB3C33326405AA CRC64;
CC -----
Query Match 55.2%; Score 550; DB 1; Length 230;
Best Local Similarity 55.3%; Pred. No. 5e-39;
Matches 109; Conservative 33; Mismatches 52; Indels 4; Gaps 3;
QY 1 OLG-ATENGLESANACPDAILFARGSTPEGNMGITVGPALANGLESHI--RNTWIOG 57
DB 30 QLGRTTRDDLNGNSACDVIPIYARGSTETNIGL-TLGPSIASNLESFAFGTGVWIOG 88
QY 58 VCGPYDAALATNPLPGTQSAINTDEGKRFLPALANQKPNTPVWAGYSQGAALIAAAVSE 117
DB 89 VGYAYRATLGDNALPGTSSAATREMLGLFQOANTKCPDATALAGGYSQGAALAAASIED 148
QY 118 LSGAVKEQVGKVALFGYTONLQNRGGIANYPRERTKVFQCNVGDAVCTGTLLIIPAHLSYT 177
DB 149 LDSAIRDKIAGTVLFGYTKNLQNRGRIPNYPADRTKVFQCNVGLDCTGSLIVAAPHLAYG 208
QY 178 IEARGEANRFLDRIRA 194
DB 209 PDARGPAPEFLIEKVRA 225
RESULT 10
CUTII_FUSSO STANDARD; PRT; 230 AA.
ID CUTII_FUSSO AC P00590;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Cutinase 1 precursor (EC 3.1.1.74) (Cutin hydrolase 1).
GN Names:CURT; Synonyms:CURTA;
OS Fusarium solani subsp. pisi (Nectria haematococca).

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
[1]
NCBI_TaxID=70791;
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC STRAIN=T-8;
RA Soliday C.L., Flurkey W.H., Okita T.W., Kolattukudy P.E.;
RT "Cloning and structure determination of cDNA for cutinase, an enzyme
involved in fungal penetration of plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3939-3943(1984).
[2]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=89137761; PubMed=2703464;
RA Soliday C.L., Dickman M.B., Kolattukudy P.E.;
RT "Structure of the cutinase gene and detection of promoter activity in
the 5'-flanking region by fungal transformation.";
RL J. Bacteriol. 171:1942-1951(1989).
[3]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
RC MEDLINE=92220194; PubMed=1560844; DOI=10.1038/356615a0;
RA Martinez C., de Geus P., Lauwers M., Matthysens G., Cambillau C.;
RT "Fusarium solani cutinase is a lipolytic enzyme with a catalytic
serine accessible to solvent.";
RL Nature 356:615-618(1992).
[4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RC MEDLINE=94114517; PubMed=8286366;
RA Martinez C., Nicolas A., van Tilbeurgh H., Egloff M.-P., Cudrey C.,
Verger R., Cambillau C.;
RT "Cutinase, a lipolytic enzyme with a preformed oxyanion hole.";
RL Biochemistry 33:83-89(1994).
[5]
RP X-RAY CRYSTALLOGRAPHY (1.0 ANGSTROMS).
RC MEDLINE=97318923; PubMed=9175860; DOI=10.1006/jmbi.1997.1000;
RA Longhi S., Czjzek M., Lanzin V., Nicolas A., Cambillau C.;
RT "Atomic resolution (1.0 A) crystal structure of *Fusarium solani*
cutinase: stereochemical analysis.";
RL J. Mol. Biol. 268:779-799(1997).
[6]
RP X-RAY CRYSTALLOGRAPHY (1.15 ANGSTROMS) OF 33-230.
RA Nicolas A., Martinez C., Cambillau C.;
RL Submitted (MAR-1997) to the PDB data bank.
[7]
RP STRUCTURE BY NMR.
RC MEDLINE=98046750; PubMed=9385640;
RA Prompers J.J., Groenewegen A., van Schaik R.C., Pepermans H.A.M.,
Hilbers C.W.;
RT "1H, 13C, and 15N resonance assignments of *Fusarium solani* pisi
cutinase and preliminary features of the structure in solution.";
RL Protein Sci. 6:2375-2384(1997).
CC -1- FUNCTION: Catalyzes the hydrolysis of cutin, a polyester that
forms the structure of plant cuticle. Allows pathogenic fungi to
penetrate through the cuticular barrier into the host plant during
the initial stage of the fungal infection.
CC -1- CATALYTIC ACTIVITY: Cutin + H(2)O = cutin monomers.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- INDUCTION: By contact with cutin.
CC -1- PM: The 2 disulfide bonds play a critical role in holding the
catalytic residues in juxta-position; reduction of the disulfide
bridges results in the complete inactivation of the enzyme.
CC -1- SIMILARITY: Belongs to the cutinase family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; K02640; AAA33334.1; -; mRNA.
CC EMBL; M29759; AAA33335.1; -; Genomic_DNA.
CC PIR; A32836; UVFUS.
CC PDB; 1AGY; X-ray; @=31-230.
CC PDB; 1CEX; X-ray; @=17-230.

Query Match 54.7%; Score 545; DB 1; Length 230;
Best Local Similarity 54.8%; Pred. No. 1.3e-38;
Matches 108; Conservative 32; Mismatches 53; Indels 4; Gaps 3

Qy 1 QLG-AIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHI--RNWIQ 57
Db 30 QLGRITDDLLINGSASCRDVIYARGSTETGNLG-TLGFSTASNLSEAFGKGVW 88
Qy 58 VGGPYDAALATNPLPRGTSQANIDEGKRLPALANQKPNTPVVGYSQGAALIAAVSE 117
Db 89 VGGAYRATLGDNALPRGTSAAIREMLGLFQANTKCPDNLTIAGGYSQGAALAAASIED 148
Qy 118 LSGAVKEQVGVAFQYTONLQNRGGIANYPRRTKFCVNGDAVCTGTLITPAHLSYT 177
Db 149 LDSAIRDKIAGTVLFGYTKNLQNRGIPNYPADRTKVCNTGDLVCTGSLIAPAHLAYG 208
Qy 178 IEARGEAREFLDRIRA 194
Db 209 PDARGPAPEFLIEKVRA 225

RESULT 11
Q4IH51 GIBZE
ID Q4IH51_GIBZE PRELIMINARY; PRT; 231 AA.
AC Q4IH51;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=FG03457.1;
OS Gibberella zeae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Atachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA Choepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kanat A., Karatas A.,
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Maucelli E., McCarthy M., Meldrim J., Meneus L.,
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Snitrov S.,
RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,

PDB; 1CUA; X-ray; @=17-230.
PDB; 1CUB; X-ray; @=17-230.
PDB; 1CUC; X-ray; @=17-230.
PDB; 1CUD; X-ray; A/B/C=17-230.
PDB; 1CUE; X-ray; @=33-229.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
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PDB; 1CUE; X-ray; @=17-230.
PDB; 1CUF; X-ray; @=17-230.
PDB; 1CUG; X-ray; @=17-230.
PDB; 1CUH; X-ray; @=17-230.
PDB; 1CUI; X-ray; @=17-230.
PDB; 1CUJ; X-ray; @=17-230.
PDB; 1CUS; X-ray; @=31-230.
PDB; 1CUT; X-ray; @=17-230.
PDB; 1CV; X-ray; @=17-230.
PDB; 1CW; X-ray; A/B=17-230.
PDB; 1CUX; X-ray; @=17-230.
PDB; 1CUI; X

[illegible]

RA	Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus"; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR	EMBL; AAHP01000016; EAL84469.1; -; Genomic DNA.
SQ	SEQUENCE 217 AA; 22483 MW; 10735C585B7690FA CRC64;
Query Match	49.6%; Score 494; DB 2; Length 217;
Best Local Similarity	50.8%; Pred. No. 3e-34;
Matches	98; Conservative 35; Mismatches 54; Indels 6; Gaps 3
QY	3 GATENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHIRN--IIWIQGVGG 60
Db	28 GMSSNELESG---PCRDVTTFARGSTEQNGMLIVGPGVCSSLKKDLGSKDVACQGVGG 80
QY	61 PYDAALATNPLPRGTSQANIDEGKRLPALANQKCPNTFVVAGYSQGAALIAAAVSELG 120
Db	85 AYTAQLAPNFLSQTNQASINAATDMFDLANTKCPNTKI VAGYSQGSVIDNTIQALGS 144
QY	121 AVKEQVKGVAFGYTONLQRGGIANYPRRTKVFCNVGDVCTGLTIITPAHLSTYIEA 180
Db	145 DLKAKYKGVLFGFTNRVADKGOIPGYPKDQTKIYCAVGDMVCWNTLIITPAHLTIGADA 204
QY	181 RGEAARFLRDIR 193
Db	205 -GDAAKEFLASKVQ 216
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ID	Q4WQV2 ASPFU PRELIMINARY; PRT; 214 AA.
AC	Q4WQV2;
DT	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE	Cutinase, putative.
GN	ORFNames=Afu4g14120;
OS	Aspergillus fumigatus Af293.
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX	NCBI_TaxID=330879;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=Af293;
RA	Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley., Arroya J., Berriam M., Abe K., Archer D.B., Bermejo C., Bennett J., Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S., Farman M., Fedorova N., Fedorova N., Feldblum T.V., Fischer R., Posner N., Fraser A., Garcia J.L., Garcia M.J., Goble A., Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B., Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J., Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R., Kumagai T., Lafon A., Latge J.-P., Li W., Lord A., Lu C., Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M., Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I., Penalva M.A., Perlea M., Price C., Pritchard B.L., Quail M.A., Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U., Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M., Ronning C.M., Rutter S., Salzberg S.L., Sanchez M., Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S., Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus"; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

RA	Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus"; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR	EMBL; AAHP01000016; EAL84469.1; -; Genomic DNA.
SQ	SEQUENCE 217 AA; 22483 MW; 10735C585B7690FA CRC64;
Query Match	49.6%; Score 494; DB 2; Length 217;
Best Local Similarity	50.8%; Pred. No. 3e-34;
Matches	98; Conservative 35; Mismatches 54; Indels 6; Gaps 3
QY	3 GATENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHIRN--IIWIQGVGG 60
Db	28 GMSSNELESG---PCRDVTTFARGSTEQNGMLIVGPGVCSSLKKDLGSKDVACQGVGG 80
QY	61 PYDAALATNPLPRGTSQANIDEGKRLPALANQKCPNTFVVAGYSQGAALIAAAVSELG 120
Db	85 AYTAQLAPNFLSQTNQASINAATDMFDLANTKCPNTKI VAGYSQGSVIDNTIQALGS 144
QY	121 AVKEQVKGVAFGYTONLQRGGIANYPRRTKVFCNVGDVCTGLTIITPAHLSTYIEA 180
Db	145 DLKAKYKGVLFGFTNRVADKGOIPGYPKDQTKIYCAVGDMVCWNTLIITPAHLTIGADA 204
QY	181 RGEAARFLRDIR 193
Db	205 -GDAAKEFLASKVQ 216
RESULT 15	
Q4WQV2 ASPFU	
ID	Q4WQV2 ASPFU PRELIMINARY; PRT; 214 AA.
AC	Q4WQV2;
DT	13-SEP-2005 (TrEMBLrel. 31, Created)
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE	Cutinase, putative.
GN	ORFNames=Afu4g14120;
OS	Aspergillus fumigatus Af293.
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX	NCBI_TaxID=330879;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=Af293;
RA	Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley., Arroya J., Berriam M., Abe K., Archer D.B., Bermejo C., Bennett J., Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S., Farman M., Fedorova N., Fedorova N., Feldblum T.V., Fischer R., Posner N., Fraser A., Garcia J.L., Garcia M.J., Goble A., Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B., Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J., Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R., Kumagai T., Lafon A., Latge J.-P., Li W., Lord A., Lu C., Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M., Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I., Penalva M.A., Perlea M., Price C., Pritchard B.L., Quail M.A., Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U., Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M., Ronning C.M., Rutter S., Salzberg S.L., Sanchez M., Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S., Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus"; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

RA	Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J., White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K., Machida M., Hall N., Barrell B., Denning D.W.; "Genomic sequence of the pathogenic and allergenic filamentous fungus Aspergillus fumigatus"; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC	-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
DR	EMBL; AF417005; AAL18697.1; -; Genomic_DNA.
DR	HSSP; P00590; 2CUT.
DR	SWR; Q96US9; 35-230.
DR	InterPro; IPR000675; Cutinase.
DR	InterPro; IPR011150; Cutinase_monf.
DR	Pfam; PF01083; Cutinase; 1.
DR	PRINTS; PRSF000861; Cutinase; 1.
DR	PROSITE; PS00129; CUTINASE.
DR	PROSITE; PS00155; CUTINASE_1; 1.
DR	PROSITE; PS00931; CUTINASE_2; 1.
KW	Hydrolase; Serine esterase; Signal.
FT	SIGNAL 1 16 Potential.
FT	CHAIN 17 231 Cutinase 3.
FT	ACT SITE 137 137 By similarity.
FT	ACT SITE 192 192 By similarity.
FT	ACT SITE 205 205 By similarity.
FT	


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CC preliminary data.
DR EMBL; AAHF0100005; EAL89382.1; -; Genomic DNA.
SQ SEQUENCE 214 AA; 22325 MW; C0B300C69C56CB63 CRC64;

Query Match 46.9%; Score 467.5; DB 2; Length 214;
Best Local Similarity 49.7%; Pred. No. 5.5e-32;
Matches 96; Conservative 30; Mismatches 62; Indels 5; Gaps 3;

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Db 23 ERLSSGNELRNGACKPITFI PARASTEFGLMGLSTGPAVCNSLKAAPQVACQGVGPA 82
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 62 YDAALATNPLPRGTSQANTDEGKRLPALANQKCPNTPVWAGYSQGAALIAAIVSELGA 121
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 83 YTADLASNALPENTSOAINAEAMELFPQAASKCPDTQIVAGGYSQGTAVMDGSIKRLPEE 142
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QY 122 VKEQVKGVALFGYTONLQNRGGIANYPREBTKVFCNVGDVAVCTGTLLIITPAHLSYTIAR 181
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 143 VKERINGVVLFGYTRNAQERGQIANPPKQVKIYCAWGDVCDGTLIVITAAHFTYGANT- 201
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QY 182 GEAAARFLDRDIRA 194
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Db 202 GDAARFLGKLT 214
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Search completed: February 4, 2006, 04:56:11
Job time : 256 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2006, 04:56:24 ; Search time 48 Seconds
(without alignments)
334.148 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESANACPDPA.....SYTIARGEARFLRDRIRA 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/RE_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	991	99.5	194	2	US-09-873-075A-1
2	991	99.5	229	1	US-08-817-997A-2
3	500.5	50.3	231	2	US-09-177-234-3
4	499.5	50.2	232	2	US-09-177-234-8
5	482	48.4	232	2	US-09-177-234-6
6	260	26.1	255	2	US-09-585-468-1
7	260	26.1	255	2	US-10-114-115A-1
8	260	26.1	255	2	US-10-114-116-1
9	260	26.1	255	2	US-10-231-478-1
10	189.5	19.0	217	2	US-09-050-739-10
11	188.5	18.9	219	2	US-09-050-739-14
12	178	17.9	226	2	US-09-050-739-52
13	167.5	16.8	262	2	US-09-050-739-56
14	140	14.1	285	2	US-09-095-855-197
15	140	14.1	285	2	US-09-205-426-197
16	117	11.7	748	1	US-08-997-080-154
17	117	11.7	748	1	US-08-997-362-154
18	117	11.7	748	2	US-09-095-855-154
19	117	11.7	748	2	US-09-324-542-154
20	117	11.7	748	2	US-09-205-426-154
21	116	11.6	167	1	US-08-997-080-112
22	116	11.6	167	1	US-08-997-362-112
23	116	11.6	167	2	US-09-095-855-112
24	116	11.6	167	2	US-09-324-542-112
25	116	11.6	167	2	US-09-205-426-112
26	114.5	11.5	28	1	US-08-817-997A-3
27	88	8.8	1385	2	US-09-252-991A-21919

28	87	8.7	4550	1	US-08-804-227C-8	Sequence 8, Appli
29	87	8.7	4550	1	US-08-804-198-2	Sequence 2, Appli
30	86	8.6	357	2	US-09-583-110-3238	Sequence 3238, Ap
31	86	8.6	370	2	US-09-107-433-3018	Sequence 3018, Ap
32	85.5	8.6	297	2	US-09-902-540-16434	Sequence 16434, A
33	82.5	8.3	666	1	US-09-252-991A-17462	Sequence 17462, A
34	81	8.1	345	1	US-08-282-197C-50	Sequence 50, Appl
35	81	8.1	592	1	US-08-217-327-8	Sequence 8, Appli
36	79.5	8.0	200	2	US-09-355-166-18	Sequence 18, Appl
37	78.5	7.9	309	2	US-09-605-703B-1240	Sequence 1240, Ap
38	78.5	7.9	309	2	US-09-605-703B-1242	Sequence 1242, Ap
39	78.5	7.9	1039	2	US-09-409-648-7	Sequence 7, Appli
40	78.5	7.9	1039	2	US-09-409-648-8	Sequence 8, Appli
41	78.5	7.9	1039	2	US-09-054-272-10	Sequence 10, Appl
42	78.5	7.9	1039	2	US-09-949-002-298	Sequence 298, App
43	78.5	7.9	1039	6	5196511-2	Patent No. 5196511
44	78	7.8	1014	2	US-09-252-991A-17583	Sequence 17583, A
45	77.5	7.8	495	2	US-09-252-991A-27501	Sequence 27501, A

ALIGNMENTS

RESULT 1

US-09-873-075A-1
; Sequence 1, Application US/09873075A
; Patent No. 6960459
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Schroder Glad, Sanne
; APPLICANT: Fukuyama, Shiro
; APPLICANT: Matsui, Tomoko
; TITLE OF INVENTION: Cutinase variants
; FILE REFERENCE: 10038.200-US
; CURRENT APPLICATION NUMBER: US/09/873, 075A
; CURRENT FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Humicola insolens
; US-09-873-075A-1

Query Match	99.5%;	Score	991;	DB 2;	Length	194;			
Best Local Similarity	99.5%;	Pred. No.	6.8e-105;						
Matches	193;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
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Db	1	QLGAIENGLESANACPDAILIFARGSTEPGNMGITVGPALANGLES	HIRNIWIOGVGG	60					
Qy	61	PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVVGAGYSGQAALIAAAVSEL	SG	120					
Db	61	PYDAALATNLFPRGTSQANIDEGKRLFALANQKCPNTPVVGAGYSGQAALIAAAVSEL	SG	120					
Qy	121	AVKEQKGVGVLFYGTQNLQNRGGIANYPRRTKVCNVDGAVCTGTLIITPAHLSYTIEA	180						
Db	121	AVKEQKGVGVLFYGTQNLQNRGGIANYPRRTKVCNVDGAVCTGTLIITPAHLSYTIEA	180						
Qy	181	RGEAARFLRDRIRA	194						
Db	181	RGEAARFLRDRIRA	194						

RESULT 2

US-08-817-997A-2

; Sequence 2, Application US/08817997A

; Patent No. 5827719

; GENERAL INFORMATION:

; APPLICANT: Sandal, Thomas

; APPLICANT: Kauppinen, Sakari

; APPLICANT: Kofod, Lene V.

RESULT 2

US-08-817-997A-2
; Sequence 2, Application US/08817997A
; Patent No. 5827719
; GENERAL INFORMATION:
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Kofod, Lene V.

; TITLE OF INVENTION: An Enzyme With Lipolytic
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58277190 No. 5827719disk Of No. 5827719th America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,997A
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 7435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4316.204
; TELEPHONE: 212-878-9652
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 229 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-08-817-997A-2
Query Match 99.5%; Score 991; DB 1; Length 229;
Best Local Similarity 99.5%; Pred. No. 8.6e-105;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLSHIRNIWQVGG 60
DB 36 QLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLSHIRNIWQVGG 95
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DB 96 PYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAASVLSG 155
QY 121 AVKEQKGVVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLLITPAHLSYTI 180
DB 156 AVKEQKGVVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLLITPAHLSYTI 215
QY 181 RGEARFLRDRI 194
DB 216 RGEARFLRDRI 229
RESULT 3
US-09-177-234-3
; Sequence 3, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Trichophaea saccata
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
;
US-09-177-234-8
Query Match 50.2%; Score 499.5; DB 2; Length 232;
Best Local Similarity 50.5%; Pred. No. 1.1e-48;
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Gliocladium sp.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
;
US-09-177-234-3
Query Match 50.3%; Score 500.5; DB 2; Length 231;
Best Local Similarity 50.0%; Pred. No. 8.8e-49;
Matches 95; Conservative 34; Mismatches 58; Indels 3; Gaps 2;
QY 5 IENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLSHIRNIWQVGGPY 62
DB 42 VRDELNRG-GSACPKAILIFARGTMELDNMGLLVGPALAGGLEGTLSNNLWVQVGGQY 100
QY 63 DAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVAVGGYSQGAALIAAASVLSGAV 122
DB 101 AANLEGNLFPDGTTPKATQEMLSLLQLADTKCPNSKIVTGGYSQGAALVAAAIKAS 160
QY 123 KEQVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLLITPAHLSYTI 182
DB 161 RQKIVGTVLFGYTKNKGQVENVSTDLRLVYCNLGDLCBGTLLIVLPPHLLYGVQAA 220
QY 183 EAARFLRDRI 192
DB 221 PAAQFLASKI 230
RESULT 4
US-09-177-234-8
; Sequence 8, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Trichophaea saccata
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(31)
;
US-09-177-234-8

QY 183 EA 184
Db 245 AA 246

RESULT 8

US-10-114-116-1

; Sequence 1, Application US/10114116

; Patent No. 6828129

; GENERAL INFORMATION:

; APPLICANT: Sumitomo Chemical Co. Ltd.

; TITLE OF INVENTION: Esterase Genes and Use thereof

; FILE REFERENCE: P150409

; CURRENT APPLICATION NUMBER: US/10/114,116

; PRIOR FILING DATE: 2002-04-03

; PRIOR APPLICATION NUMBER: US/09/585,468

; PRIOR FILING DATE: 2000-06-02

; NUMBER OF SEQ ID NOS: 5

; SEQ ID NO 1

; LENGTH: 255

; TYPE: PRT

; ORGANISM: Aspergillus flavus

US-10-114-116-1

Query Match 26.1%; Score 260; DB 2; Length 255;

Best Local Similarity 34.1%; Pred. No. 2.9e-21;

Matches 62; Conservative 30; Mismatches 70; Indels 20; Gaps 6;

QY 11 SGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHT--RNWIQVGGPYDAALAT 68

Db 77 NGFTGACTDVTYVLFARCTSEPGNVGLVGPPLAEAFEGAVGASALSFQGVNG-YASV-E 134

QY 69 NFLPRTGSQANIDEGKRLPALANO-----KCPNTPVWAGGYSGQAALIAAAVSELGAV 122

Db 135 GYLGG-----EAAGSKAMASQASDILSKCPDPTKLVMSGYSGQCOIVHNAVEQLPAEH 187

QY 123 KEQVKGVALFGYTONLQNRGGIANYPRETRKVFNCNVGDAVCTGTLLITPAHLSTYITEARG 182

Db 188 ASKISSVLLFG---DPYKGKALPNVDASRVHTVCHAGDTICENSVIILPAHLTYAVDVAS 244

QY 183 EA 184

Db 245 AA 246

RESULT 9

US-10-231-478-1

; Sequence 1, Application US/10231478

; Patent No. 6936445

; GENERAL INFORMATION:

; APPLICANT: KAWABE, TOMOYASU

; APPLICANT: KAWITAMARI, MASASHI

; TITLE OF INVENTION: ENZYME PREPARATION AND METHOD OF USING THE SAME

; FILE REFERENCE: 7372/73243

; CURRENT APPLICATION NUMBER: US/10/231,478

; CURRENT FILING DATE: 2002-12-09

; PRIOR APPLICATION NUMBER: JP 2001-265495

; PRIOR FILING DATE: 2001-09-03

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 255

; TYPE: PRT

; ORGANISM: Aspergillus flavus

US-10-231-478-1

Query Match 26.1%; Score 260; DB 2; Length 255;

Best Local Similarity 34.1%; Pred. No. 2.9e-21;

Matches 62; Conservative 30; Mismatches 70; Indels 20; Gaps 6;

QY 11 SGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHT--RNWIQVGGPYDAALAT 68

Db 77 NGFTGACTDVTYVLFARCTSEPGNVGLVGPPLAEAFEGAVGASALSFQGVNG-YASV-E 134

```
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/050,739
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: 0376/97
; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488
; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 219
; TYPE: PR1
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-14

Query Match      18.9%; Score 188.5; DB 2; Length 219;
Best Local Similarity 31.7%; Pred. No. 3.4e-13;
Matches 66; Conservative 32; Mismatches 75; Indels 35; Gaps 11;

QY      8 GLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHT-RNIWIOGVGPGYDAAL 66
      25 GAVAPATACPDAEVVFARGTPEPGIG-TVGNAFVSALRSKYNKVGTVAVKYPAD--- 80
QY      67 ATNFLPRGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGA---LIAAAVSELGAVK 123
      81 --NQIDVGAN---DMSAHQSWAN-SCPNTRLVPGGSLGAAVTDVLAAPTQMGFTN 133
QY      124 -----EQVGVALFGYTONLQNRGGIANYP---ERTKVFNCNVGDAVCTGLIIT--- 170
      134 PLPPGSDHEIAAVALFG---NGSQWGPITNFSPAYNDRITELCHGDDPVCHPADPNTWEA 191
QY      171 --PAHLSYTIETARG---EAAFLRDRIR 193
      192 NWPQHLAGAYVSGWMVQAADFVAGKIQ 219

RESULT 12
US-09-050-739-52
; Sequence 52, Application US/09050739
; Patent No. 6641814
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/050,739
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: 0376/97
; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488
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; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 226
; TYPE: PR1
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-52

Query Match      17.9%; Score 178; DB 2; Length 226;
Best Local Similarity 33.2%; Pred. No. 5.6e-12;
Matches 64; Conservative 24; Mismatches 75; Indels 30; Gaps 11;

QY      17 CPDAILIFARGSTPEGNMGITVGPALANGLESHT-RNIWIOGVGPGYDAALATNPLPRGT 75
      47 CPDAEVVFARGTPEPGIG-RVQAQFVSLRQQTNKSGTGVNYPANG---DFLAAAD 101
QY      76 SQANIDEGKRLFALANQKCPNTPVVAGGYSQGA---LIAAA-----VSELGAVKEQ 125
      102 GANDASDHIOQMASA---CRATRLVLGGYSQGAVIDIVTAAPLPGLGFTQPLPPAADH 158
QY      126 VKGVALFGYTONLQNRGG---IANYPR---ERTKVFNCNVGDAVCT-GTLIITPAHLSYTIIE 179
      159 IAAIALFG---NPSGRAGGLMSALTPOFGSKTINLCNNGDPICSDGNR---WRAHLGYVPG 213
QY      180 ARGEAARFLDRIR 192
      214 MTNQAAARFVASRI 226

RESULT 13
US-09-050-739-56
; Sequence 56, Application US/09050739
; Patent No. 6641814
; GENERAL INFORMATION:
; APPLICANT: ANDERSEN, Peter
; APPLICANT: NIELSEN, Rikke
; APPLICANT: OETTINGER, Thomas
; APPLICANT: RASMUSSEN, Peter Birk
; APPLICANT: ROSENKRANDS, Ida
; APPLICANT: WELDINGH, Karin
; APPLICANT: FLORIO, Walter
; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
; FILE REFERENCE: 670001-2002.1
; CURRENT APPLICATION NUMBER: US/09/050,739
; CURRENT FILING DATE: 1998-03-30
; EARLIER APPLICATION NUMBER: 0376/97
; EARLIER FILING DATE: 1997-04-02
; EARLIER APPLICATION NUMBER: 1277/97
; EARLIER FILING DATE: 1997-11-10
; EARLIER APPLICATION NUMBER: 60/044,624
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: 60/070,488
; EARLIER FILING DATE: 1998-01-05
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 262
; TYPE: PR1
; ORGANISM: Mycobacterium tuberculosis
US-09-050-739-56

Query Match      16.8%; Score 167.5; DB 2; Length 262;
Best Local Similarity 31.8%; Pred. No. 1.1e-10;
Matches 67; Conservative 22; Mismatches 69; Indels 53; Gaps 12;

QY      14 ANACPDAILIFARGSTPEGNMGITVGPALANGLESHTIRNINWIOGVG---GPYDAALATNF 70
      41 ADGCPDAEVTFARGTPEPGIG-RVQAQFVDSL-----QQTGMIGIVPVVVASR 91
QY      71 LP-RGTSQANIDEGKRLFALANQKCPNTPVVAGGYSQGAAL---IAAAV-----SELS 119
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Db 92 LQHGDDGAN-DAISHIKSMAS-SCNTKVLGGYSQGATVTDIVAGVPLGSGISFGSPLP 149
QY 120 GAVKEQVKGVALFGYTONLQNRGG-----IANYPRERTKVFNCVGDVACTGTLITPAHL 174
Db 150 AAYADNVAAVVFG---NPSNRAGGSSLSPLFGSKAIDLCLNPTDPICTIC-----HV 197
QY 175 SVTIBARG-----EAFRLDRIRA 194
Db 198 GPGNEFSGHIDGYIPTTYTTOAASFVQVRLRA 228

RESULT 14

US-09-095-855-197
; Sequence 197, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITL OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:

INFORMATION FOR SEQ ID NO: 197:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 285 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-095-855-197

Query Match 14.1%; Score 140; DB 2; Length 285;
Best Local Similarity 29.2%; Pred. No. 1.7e-07;
Matches 62; Conservative 30; Mismatches 68; Indels 52; Gaps 15;
QY 9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHERINIWIQGVGGPYDAALA 67
Db 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WGDAFVNALRPKVGE---QSVG-----TYA 76
QY 68 TNF-----LPRGTSQANIDEGKRLFALANOKCPNTPWAGGYSQGAALIAAAV--- 115

Db 77 VNYPAGEFDFKSAAPMGAADAS---GRVQWADN---CPDTKLVLGMSQAGVIDLITVDP 131
QY 116 -----SELGAVKEQVKGVALFGYTONLQNRGG-----IANYPRERTKVFNCVGD 161
Db 132 RPLGRFTPTMPPRVADHVAAVVFG--NPLRDIRGGGGLPQMSTGYGPKSIDLCALDDP 189
QY 162 VCTGTLLITPAHLSYT-----IEARGEAAARFLR 189
Db 190 FCSPGFNL-PAHFAYADNGMVE---EAAAFAR 217

RESULT 15

US-09-426-197
; Sequence 197, Application US/09205426
; Patent No. 6406704

GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITL OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 197
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-205-426-197

Query Match 14.1%; Score 140; DB 2; Length 285;
Best Local Similarity 29.2%; Pred. No. 1.7e-07;
Matches 62; Conservative 30; Mismatches 68; Indels 52; Gaps 15;

QY 9 LESGSANACPDAILIFARGS-TEPGNMGITVGPALANGLESHERINIWIQGVGGPYDAALA 67
Db 27 IPTASADPCPDIEVIFARGTGAEPG-LG-WGDAFVNALRPKVGE---QSVG-----TYA 76
QY 68 TNF-----LPRGTSQANIDEGKRLFALANOKCPNTPWAGGYSQGAALIAAAV--- 115
Db 77 VNYPAGEFDFKSAAPMGAADAS---GRVQWADN---CPDTKLVLGMSQAGVIDLITVDP 131
QY 116 -----SELGAVKEQVKGVALFGYTONLQNRGG-----IANYPRERTKVFNCVGD 161
Db 132 RPLGRFTPTMPPRVADHVAAVVFG--NPLRDIRGGGGLPQMSTGYGPKSIDLCALDDP 189
QY 162 VCTGTLLITPAHLSYT-----IEARGEAAARFLR 189
Db 190 FCSPGFNL-PAHFAYADNGMVE---EAAAFAR 217

Search completed: February 4, 2006, 04:57:52
Job time : 49 secs


```
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Stickies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/152,300
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Humicola insolens
US-10-152-300-1

Query Match      99.5%; Score 991; DB 4; Length 194;
Best Local Similarity 99.5%; Pred. No. 8.8e-95;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIQVGG 60
Db      1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIQVGG 60

QY      61 PYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAASVLSG 120
Db      61 PYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAASVLSG 120

QY      121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGTLIITPAHLSYTTIEA 180
Db      121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGTLIITPAHLSYTTIEA 180

QY      181 RGEAARFLDRIRA 194
Db      181 RGEAARFLDRIRA 194

RESULT 3
US-10-846-123-1
; Sequence 1, Application US/10846123
; Publication No. US20040226672A1
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Stickies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/846,123
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US/10/152,300
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Humicola insolens
US-10-846-123-1

Query Match      99.5%; Score 991; DB 5; Length 194;
Best Local Similarity 99.5%; Pred. No. 8.8e-95;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIQVGG 60
Db      1 QLGAIENGLESGSANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIQVGG 60

QY      61 PYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAASVLSG 120
Db      61 PYDAALATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAASVLSG 120

QY      121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGTLIITPAHLSYTTIEA 180
Db      121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGTLIITPAHLSYTTIEA 180

QY      181 RGEAARFLDRIRA 194
Db      181 RGEAARFLDRIRA 194

RESULT 4
US-10-152-300-2
; Sequence 2, Application US/10152300
; Publication No. US20030051836A1
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Lund, Henrik
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Stickies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/152,300
; CURRENT FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Fusarium solani pisi
US-10-152-300-2

Query Match      54.5%; Score 542.5; DB 4; Length 199;
Best Local Similarity 55.9%; Pred. No. 4.9e-48;
Matches 105; Conservative 31; Mismatches 49; Indels 3; Gaps 2;

QY      9 LEGSANACPDAILIFARGSTPGNMGITVGPALANGLESIRNIWIQVGGPYDAAL 66
Db      8 LINGSASCADVIPIYARGSTETCNLG-TLGPSIASNLSEAFGKDGVWIQVGGAYRATL 66

QY      67 ATNPLPGTSGQANIDEGKRLFALANQKCPNTPVVAGGYSQGAALIAAASVLSGAVKEQV 126
Db      67 GDNALPRGTSSAATREMLGLFQQANTKCPDYLATAGGYSQGAALAAASIEDLSAIRDKI 126

QY      127 KGVALFGYTONLQNRGGIANYPRRTKVCNVDGAVCTGTLIITPAHLSYTTIEARGEAA 186
Db      127 AGTVLFGYTKNLQNRGRIPNYPADRTKVCNCTGDLVCTGSLIVAAPHLAYGPDARGPAPE 186

QY      187 FLDRIRA 194
Db      187 FLIEKVRA 194

RESULT 5
US-10-846-123-2
; Sequence 2, Application US/10846123
; Publication No. US20040226672A1
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Lund, Henrik
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Stickies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/846,123
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US/10/152,300
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
```


; APPLICANT: RASMUSSEN, Peter Birk
 ; APPLICANT: ROSENKRANDS, Ida
 ; APPLICANT: WELDINGH, Karin
 ; APPLICANT: FLORIO, Walter
 ; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
 ; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS
 ; FILE REFERENCE: 670001-2002.1
 ; CURRENT APPLICATION NUMBER: US/09/791,171
 ; CURRENT FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 09/050,739
 ; PRIOR FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 0376/97
 ; PRIOR FILING DATE: 1997-04-02
 ; PRIOR APPLICATION NUMBER: 1277/97
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/044,624
 ; PRIOR FILING DATE: 1997-04-18
 ; PRIOR APPLICATION NUMBER: 60/070,488
 ; PRIOR FILING DATE: 1998-01-05
 ; NUMBER OF SEQ ID NOS: 173
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 217
 ; TYPE: PR1
 ; ORGANISM: Mycobacterium tuberculosis
 US-09-791-171-10

 Query Match 19.0%; Score 189.5; DB 3; Length 217;
 Best Local Similarity 30.8%; Pred. No. 3.3e-11;
 Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

 QY 8 GLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIQVGGPYDAALA 67
 DB 26 GGRAAHADPCSDIAVVFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSIGVYA 76

 QY 68 TNFLP-----RGTSQANIDEGKRLFALANQKCPNTVPVAGGYSQGAALIAAAVSELGAVK 123
 DB 77 VNYPASDDYRASASNGSDASAHIQRTVASCNTRIVLGGYSQGAATVIDLSTAMP PAVA 136

 QY 124 EQVKGVALF-----GYTONLQNRGG---IANYPRERTKVCNVDGAVCTGTTLITPAHLS 175
 DB 137 DHVAALVALFGEPPSGFSSMLWGGSLPTIGPLYSSKTNILCAPDDPCTGGNIM-AHVS 195

 QY 176 YTIEA-RGEAARFLRDRI 192
 DB 196 YVQSGMTSQAATFAANRL 213

 RESULT_13
 US-09-804-980-10
 ; Sequence 10, Application US/09804980
 ; Publication No. US20030147897A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Statens Serum Institut
 ; APPLICANT: Anderson, Peter
 ; TITLE OF INVENTION: M. Tuberculosis Antigens
 ; FILE REFERENCE: 670001-2002.4
 ; CURRENT APPLICATION NUMBER: US/09/804,980
 ; CURRENT FILING DATE: 2001-03-12
 ; NUMBER OF SEQ ID NOS: 257
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 217
 ; TYPE: PR1
 ; ORGANISM: Mycobacterium tuberculosis
 US-09-804-980-10

 Query Match 19.0%; Score 189.5; DB 3; Length 217;
 Best Local Similarity 30.8%; Pred. No. 3.3e-11;
 Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

 QY 8 GLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESIRNIWIQVGGPYDAALA 67

```
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: COGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 259
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-855-604-259
```

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Query Match          19.0%; Score 189.5; DB 3; Length 217;
Best Local Similarity 30.8%; Pred.No. 3.3e-11;
Matches 61; Conservative 25; Mismatches 89; Indels 23; Gaps 7;

QY      8 GLESGSANCPDAILIFARGSTPEGNMGITVGPALANGLESHIRNIWIQGVGGPYDAALA 67
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      26 GGRAHADPCSDIADVAFKTHQASGLG-DVGEAFVDSLTSQ-----VGGRSIGVYA 76
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      68 TNFLP----RGTSQANIDEGKRLFALANQKPNTPVVGYSQGAALIAAAVSELSGAVK 123
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      77 VNVPSDDYRASASNGSDDASAHIQRTVASCNPTRIVLGGYSQGATVIDLSTSAMPPAVA 136
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      124 EQVKGVALF-----GYTONLQNRGG---IANYPRRTKVCNVGDVCTGTLITPAHLS 175
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      137 DHVAVALFGEPSGSSFMWGGSLFTTIGPLYSKTNILCAPDDPCTCTGGNIM-AHVS 195
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      176 YTIEA-RGEAARELRDRI 192
Db      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Search completed: February 4, 2006, 05:11:43
Job time : 178 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 05:08:55 ; Search time 15 Seconds
(without alignments)
151.554 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229
Perfect score: 996
Sequence: 1 QLGATENGLESGSANACPD.....SYTIARGEARFLRDRI 194

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA_New.*
- 1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	189.5	19.0	217	7	US-11-052-554A-331
2	82.5	8.3	138	6	US-10-467-657-2928
3	79.5	8.0	200	7	US-11-179-977-18
4	79	7.9	630	6	US-10-517-939-42
5	77	7.7	575	7	US-11-185-342-3
6	76.5	7.7	436	6	US-10-467-657-7578
7	76.5	7.7	7968	7	US-11-143-980-49
8	76	7.6	710	7	US-11-143-980-40
9	75.5	7.6	1889	7	US-11-102-476-46
10	75	7.5	481	6	US-10-467-657-4396
11	75	7.5	575	7	US-11-185-342-19
12	75	7.5	575	7	US-11-185-342-21
13	74.5	7.5	463	6	US-10-531-844-2
14	74	7.4	424	7	US-11-138-642-13
15	74	7.4	424	7	US-11-047-383-10
16	74	7.4	424	7	US-11-138-882-13
17	73.5	7.4	506	6	US-10-641-678-69
18	73	7.3	1013	7	US-11-103-957-9
19	73	7.3	1531	7	US-11-103-957-15
20	72.5	7.3	592	6	US-10-467-657-550
21	72	7.2	1571	7	US-11-052-554A-2
22	71.5	7.2	1438	6	US-10-453-372-796
23	71	7.1	463	7	US-11-052-554A-261
24	70.5	7.1	250	7	US-11-054-515-73
25	70.5	7.1	1225	6	US-10-453-372-798

ALIGNMENTS

RESULT 1

US-11-052-554A-331
; Sequence 331, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:

; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR FILING DATE: 2004-07-20
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 331
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis H37Rv

Query Match	19.0%	Score	189.5;	DB	7;	Length	217;
Best Local Similarity	30.8%	Pred. No.	3.4e-11;				
Matches	61;	Conservative	25;	Mismatches	89;	Indels	23;
Gaps	7;						
Qy	8	GLESGSANACPDAILIPARGSTFPCNMGITVGPALANGLESIRNIWIQVGGPYDAALA	67				
Db	26	GGRAAHADPCSDIAVWFARGTHQASGLG-DVGEAFVDSLTSQ-----VGRSGTGVTA	76				
Qy	68	TNELP----RGTQANIDEGKRLPALANQKCPNTPVAGGYSQGAALIAAAVSELSGAVK	123				
Db	77	VNPASDDYRASANGSDSAHIQRTVASCPNTVILGGYSQGATVLDLSTAMPNVA	136				
Qy	124	EQVKGVALF-----GYTONLQNRGG---IANYPRRTKVFNCVNGDAVCTGTTLITPAHLS	175				
Db	137	DHVAVALFGPSSGFSMLWGGGSLPTIGLYSSKTNLNCAPDDPCTGGGNIM-AHVS	195				
Qy	176	YTIEA-RGEAARFLRDRI	192				
Db	196	YVQSGMTSQAATFAANRL	213				

RESULT 2

US-10-467-657-2928
; Sequence 2928, Application US/10467657
; Publication No. US20050260581A1

```

; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: CB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2928
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2928

Query Match      8.3%; Score 82.5; DB 6; Length 138;
Best Local Similarity 29.3%; Pred. No. 0.33;
Matches 36; Conservative 18; Mismatches 36; Indels 31; Gaps 8;

QY 27 GSTEPCGNGITVG-----PA-LANGLESHIRNIWQGV-----GGPYDAALATNPLP 72
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 19 GCSKGNAGFLVGGQILVASGQPAETENGCIQRLNILLQVFMVQDEPYIA--VTCFL- 75
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 73 RGTSONIDEGKRLFALANQKCNTPVAGGYSQGAALIAAAVSELGAVKEQVKGVALF 132
   :::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 76 --QTASGVQVGLRL-----DVECPHFPPVACGLCEKGVSWVA-----GGAVQR----IAAF 121
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 133 G 133
Db 122 G 122

RESULT 3
US-11-179-977-18
; Sequence 18, Application US/11179977
; Publication No. US20050249789A1
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
; FILE REFERENCE: GC511-PCT
; CURRENT APPLICATION NUMBER: US/11/179,977
; CURRENT FILING DATE: 2005-07-12
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Bacillus
US-11-179-977-18

Query Match      8.0%; Score 79.5; DB 7; Length 200;
Best Local Similarity 22.9%; Pred. No. 1;
Matches 47; Conservative 20; Mismatches 63; Indels 75; Gaps 9;

QY 3 GAIEGLSGSANACPDAILIFARGSTPEPGNMGITVGPALANGLESHIRNIWQVGGPY 62
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 21 GGNHDLISLGRIDPDAILLVGRS-----VLENGMPRFKEL-SEGVDK 67
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 63 DAALAT-----NFLPRGTSONIDEGKRLFALANQKCNTPVAGGYSQGAALIAAAVSEL 118
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 68 DLVVRTRELKDFIDEAAETHQFNRR-----VIAVGSNGANIAAS----- 108
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 119 SGAVKEQVKGVALFGYTONLQNRGGIANYPRERTK-----VFCNVG--DAVCTG 165
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 109 -----LLFHYKDVIL--KGAILHHPVPIRGIELPDMAGLPVFIGAGKYDPLCTK 155
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 166 TLIIPTAHLSTYTTEARCEAAARELRD 190
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Db 156 -----EESBELRYLRD 167

RESULT 4
US-10-517-939-42
; Sequence 42, Application US/10517939
; Publication No. US2006000343A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff
; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 630
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample
; NAME/KEY: SIGNAL
; LOCATION: (1)...(37)
US-10-517-939-42

Query Match      7.9%; Score 79; DB 6; Length 630;
Best Local Similarity 24.3%; Pred. No. 5.2;
Matches 42; Conservative 19; Mismatches 70; Indels 42; Gaps 8;

QY 15 NACPDAILIFARGSTPEPGNMGITVGPALANGLESHIRNIWQVGGPY-DAAL----- 66
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 408 NNIPVKARTFVWGAQSPAWLNNLSGPEVAVEIEQ-----WIRDYCTRYPTDAMIDVNEA 462
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 67 ATNPLPRGTSONIDEG--KELEFALANQKCNTPVAVGY-----SOGAA 109
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 463 VPGHOPAGYAOARAFGNWNIQVFLARQYCPNSIILINDYNNIRWQHNEFIALAKAQNY 522
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 110 LIAAAVS--ELSGAVKEQVKGVALFGYTONLQNRGGIANYPRERTKVFNCVNG 160
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 523 IDAVGLQAHLEKGMTAAQVKT-----IDNIWNQVKGPIYISE-----YDIGD 565
   |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 5
US-11-185-342-3
; Sequence 3, Application US/11185342
; Publication No. US20060021093A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Philip E.
; APPLICANT: Hinson, Todd K.
; APPLICANT: Carr, Brian
; APPLICANT: Duck, Nicholas B.
; TITLE OF INVENTION: GPC-1 GENES CONFERRING HERBICIDE
; FILE REFERENCE: 045600/275114
; CURRENT APPLICATION NUMBER: US/11/185,342
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: US/10/796,953
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: 60/453,237
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 21
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Db 184 GADPSG-QDSTQAFDAIAA-AQGGVWIPPGDYRLT---SSLNG-----VQNVTLQAG 234
QY 60 GPYDAALATNPLRGTSQANID-EGKRLFALANQKCPNTP--VVAGYSGQAALIAAAS 116
Db 235 SMHSVHTSRFIDQSSSSGVHVKDFAVIGETVERVDSNPDNFVNGSLGPG-----S 286
QY 117 ELSGAVKEQVK-GVALFGYTONI-----QNRGGIANYPRRTKVKFCNVGD 160
Db 287 SVSGMWLOHLKVLGWLGMNNDNLVVENRFLDMTADGLNLNGSAKVRVRNFRNQGD 345

RESULT 9
US-11-102-476-46
; Sequence 46, Application US/11102476
; Publication No. US20050271680A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Pu
; APPLICANT: Palaniappan, Raghavan U.M.
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Novel Immunogenic Proteins of Leptospira
; FILE REFERENCE: 1153.080US1
; CURRENT APPLICATION NUMBER: US/11/102,476
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: PCT/US2003/32385
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/417721
; PRIOR FILING DATE: 2002-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 1889
; TYPE: PRT
; ORGANISM: Leptospira interrogans
US-11-102-476-46

Query Match 7.6%; Score 75.5; DB 7; Length 1889;
Best Local Similarity 19.1%; Pred. No. 47;
Matches 49; Conservative 35; Mismatches 73; Indels 99; Gaps 9;
QY 8 GLESGSANACPDAILIFARGSTPEGNGMITVGPALANGLESHIRNIWQVGGPYDAALA 67
Db 110 GITSGSS-----IIKAYNGLYSEQKITVTFAILNSIQV-----TSLE 147
QY 68 TNPLRGTSQANIDEGKRLFAL-----ANQKCPNTPV-----AGGY 104
Db 148 SGLPKGTN-----RLSAIGFSDGSHQDISNDPLIYWSSNPDLVQVDDSGLASGI 200
QY 105 SOGAALIAAASVLSGAVKEQVKGVALFGYVQ-----136
Db 201 NLGTAHIRASFQSKQGA-BEMTVGDAVLSQIQVTSNNLNIPLGKKQKLTATGIYSDNSNR 259
QY 137 -----NLQNRGGIANYPRRTKVKFCNVGDVCTGTTLITPAHL-SYVIE 179
Db 260 DISSSVIWNSSNSTIANIQNGILETADTGIVTSASTENIIGSVKLIVTPAALVSISVS 319
QY 180 -ARGEAAARFLDRIRA 194
Db 320 PTNSTVAKGLQENFKA 335

RESULT 10
US-10-467-657-4396
; Sequence 4396, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4396
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4396

Query Match 7.5%; Score 75; DB 6; Length 481;
Best Local Similarity 22.9%; Pred. No. 8.8;
Matches 48; Conservative 24; Mismatches 82; Indels 56; Gaps 10;
QY 1 QLGAI-----NGLESGSANACPDAILIFARGSTE---PGNMGITVGPALA-- 43
Db 17 QISAVELASAVLAAIAEKNPALNGVITIDQDKTLAEARAADERIAQGNASALTGVVPVAYK 76
QY 44 -----NGLESHIRNIWQVGGPYDAALATNPLFRG---TSQANIDEGKRLFALAN---- 91
Db 77 DIFCQTCWRSACASAKMLDNFIFFYTATVQVQLLDGEMVTLGRTNMDE----FAMGSTNEN 132
QY 92 -----QKCP-NTPVWAGYSGQAALIAAA-----VSELGAVKEQVKGVALFGV--TQ 136
Db 133 SFYGAANKPNWPEHPVGGSSGSAVVAARLAPALGSDTGGSIQRPASHCGITGKPTY 192
QY 137 NLQNRGGIANY-----PRRTKVKFCNV 158
Db 193 GTVSRFCMWAVAYSSFDQAGPMAQTAECAI 222

RESULT 11
US-11-185-342-19
; Sequence 19, Application US/11185342
; Publication No. US20060021093A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Philip E.
; APPLICANT: Hinson, Todd K.
; APPLICANT: Carr, Brian
; APPLICANT: Duck, Nicholas B.
; TITLE OF INVENTION: GDC-1 GENES CONFERRING HERBICIDE
; TITLE OF INVENTION: RESISTANCE
; FILE REFERENCE: 045600/275114
; CURRENT APPLICATION NUMBER: US/11/185,342
; CURRENT FILING DATE: 2005-07-20
; PRIOR APPLICATION NUMBER: US/10/796,953
; PRIOR FILING DATE: 2004-03-10
; PRIOR APPLICATION NUMBER: 60/453,237
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fungal isolate from soil sample
US-11-185-342-19

Query Match 7.5%; Score 75; DB 7; Length 575;
Best Local Similarity 26.1%; Pred. No. 11;
Matches 40; Conservative 18; Mismatches 65; Indels 30; Gaps 9;
QY 55 IQGVGGPYDAALATNPLRGTSQANIDEGKRLFALANQKCPNTPVWAGYSQ-----GAAL 110
Db 33 IHGLPGDYN-PLALDYLP-----SCGLRWGVSVEL--NAAVADGYARVKQNGALI 81
QY 111 IAAAVSELS-----GAVKEQVKGVALFGYTONLQNRGGIA---NYPRTKVKFCNVGDA 161
Db 82 TTFGVGELSAINGVAGAFSEHVPVHVIVGCCFSTASQRNGMLLHHTLGNLGNDFNIFANMSAQ 141
QY 162 V-CTGTTLITPAHL-SYVIEARGEAAAR--FLDR 191

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; NAME/KEY: misc feature
; LOCATION: (261)..(262)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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; NAME/KEY: misc feature
; LOCATION: (348)..(349)
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; LOCATION: (365)..(365)
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (380)..(380)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-531-844-2

Query Match          7.5%; Score 74.5; DB 6; Length 463;
Best Local Similarity 27.5%; Pred. No. 9.3;
Matches 36; Conservative 16; Mismatches 51; Indels 33; Gaps 7

Qy 62 YDAALATNFL--PRGTQANIDEKRLPALANQKCPNTPPVAGYSQGAALIAAAVSELS 119
Db 331 YNSKATNPLATEWALSXGFDNQKLL-----LLAGLIDXR---GNSFDELV 374

Qy 120 GAVKEQVKGVALFGYTNQLNRGGIANYPRRTKVFC-NVGDAVCTG-----TLIIT 170
Db 375 PALLGXKLKAIVLFGETK--KKLAEAAKKPNITILFAENVQTAVTIAPDYSEKDDTILLS 432

Qy 171 PAHLSY-----TIERGEA 184
Db 433 PACASWDQYPNFVERGEA 450

RESULT 14
US-11-138-642-13
; Sequence 13, Application US/11138642
; Publication No. US20050287190A1
; GENERAL INFORMATION:
; APPLICANT: DESOUZA, MERVYN L.
; APPLICANT: MESSMAN, MICHAEL A.
; TITLE OF INVENTION: METHODS OF SUPPRESSING ENDOTOXIN EFFECTS IN ANIMAL
; TITLE OF INVENTION: FEEDS CONTAINING E. COLI BIOMASS
; FILE REFERENCE: 023829-0454
; CURRENT APPLICATION NUMBER: US/11/138,642
; CURRENT FILING DATE: 2005-05-26
; PRIOR APPLICATION NUMBER: 60/575,272
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/578,092
; PRIOR FILING DATE: 2004-06-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-138-642-13

Query Match          7.4%; Score 74; DB 7; Length 424;
Best Local Similarity 23.7%; Pred. No. 9.3;
Matches 46; Conservative 28; Mismatches 70; Indels 50; Gaps 13

Qy 30 EPGNMGITVCPALANGLESIRNI--WI-----QG---VGGPYDAALATNFLPRGTSQA 78
Db 245 ESAGIATVYNQRILVRGLDYINRTVFVWNTSLSGQGVTCAGGRYD-GLVEQLGGRATPAV 303

Qy 79 NIDEG-KRLPAL---ANQKCPNTPV-----AGGYSQGAALIAAAVSELSGAVKEQVKG 128
Db 304 GFAMGLERLVLLVQAVNPEFKADPVVDIYLVASGADTQSAAM-----ALAERLDELPG 357

Qy 129 VALFGYTNQLNRGGIANYPRE-----RTKVFCNVGDA-VCTGTLLIITPAHLSYTIEA 180
Db 358 VKL-----MTNHGG-GNFKKQFARADKKGARVAVVLGSEVANGTAVVKDLR----- 403

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QY 181 RGEAARFLDRIRA 194
Db 404 SGEQTAVQDSVAA 417

RESULT 15
US-11-047-383-10
; Sequence 10, Application US/11047383
; Publication No. US20060003432A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: CLARKE, TERESA
; APPLICANT: KIMBER, MATHEW
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM ENTEROCOCCUS FAECALIS
; FILE REFERENCE: IPT-318.01
; CURRENT APPLICATION NUMBER: US/11/047,383
; CURRENT FILING DATE: 2005-01-31
; PRIOR APPLICATION NUMBER: PCT/CA03/01135
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: 60/400,435
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/453,405
; PRIOR FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-047-383-10

Query Match 7.4%; Score 74; DB 7; Length 424;
Best Local Similarity 23.7%; Pred. No. 9.3;
Matches 46; Conservative 28; Mismatches 70; Indels 50; Gaps 13;
QY 30 EPGNMGITVGPALANGLESHIRNI--WI-----QG---VGGPYDAALATNFLPRGTSQA 78
Db 245 ESAGIAYTVNQRILVRGLDYNNRTVFETVNSLSGSGQGTVCAGGRYD-GLVBQLGGRATPAV 303
QY 79 NIDEG-KRLFAL---ANQKCPNPV-----AGGYSQGAALIAAAVSELSGAVKEOVKG 128
Db 304 GFAMGLERLVLLVQAVNPFEKADPVVDIYLVASGADTQSAW-----ALAEIRLDELPG 357
QY 129 VALFGYTONLQNRGGIANYPRE-----RTKVFNCVGDG-VCTGTLLIITPAHLSYITIA 180
Db 358 VKL-----MTNHGG-GNPKKQFARADKMGARVAVVLGESEVANGTAVVKDLR----- 403
QY 181 RGEAARFLDRIRA 194
Db 404 SGEQTAVQDSVAA 417

Search completed: February 4, 2006, 05:12:05
Job time : 16 secs

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:57:14 ; Search time 600 Seconds
(without alignments)
446.832 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGATENGLESGSANACPD.....SYTIEARGEARFLDRIRA 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	996	100.0	246	18	US-08-817-997-2 Sequence 2, Appli
2	991	99.5	194	31	US-10-152-300-1 Sequence 1, Appli
3	991	99.5	194	38	US-10-846-123-1 Sequence 1, Appli
4	596	59.8	209	27	US-09-791-537-26059 Sequence 26059, A
5	593.5	59.6	228	27	US-09-791-537-32037 Sequence 32037, A
6	578	58.0	196	11	US-08-171-805-59 Sequence 59, Appl
7	578	58.0	196	15	US-08-551-983-64 Sequence 64, Appl
8	576	57.8	194	11	US-08-171-805-57 Sequence 57, Appl
9	576	57.8	194	15	US-08-551-983-62 Sequence 62, Appl
10	576	57.8	224	27	US-09-791-537-55942 Sequence 55942, A
11	576	57.8	227	37	US-10-703-032-168488 Sequence 168488, A
12	564	56.6	223	27	US-09-791-537-55932 Sequence 55932, A
13	561	56.3	194	11	US-08-171-805-58 Sequence 58, Appl
14	561	56.3	194	15	US-08-551-983-63 Sequence 63, Appl
15	554	55.6	214	27	US-09-791-537-17346 Sequence 17346, A
16	554	55.6	214	27	US-09-791-537-17351 Sequence 17351, A
17	550.5	55.3	228	27	US-09-791-537-55941 Sequence 55941, A
18	550	55.2	230	27	US-09-791-537-102891 Sequence 102891, A
19	546	54.8	214	27	US-09-791-537-132722 Sequence 132722, A
20	546	54.8	230	11	US-08-100-586-43 Sequence 43, Appl
21	546	54.8	230	27	US-09-791-537-114396 Sequence 114396, A
22	545.5	54.8	214	27	US-09-791-537-127534 Sequence 127534, A
23	545	54.7	230	27	US-09-791-537-55944 Sequence 55944, A
24	544	54.6	214	27	US-09-791-537-17344 Sequence 17344, A
25	543.5	54.6	231	37	US-10-703-032-105885 Sequence 105885, A
26	543	54.5	214	27	US-09-791-537-17380 Sequence 17380, A
27	542.5	54.5	198	11	US-08-171-805-56 Sequence 56, Appl
28	542.5	54.5	198	15	US-08-551-983-61 Sequence 61, Appl
29	542.5	54.5	198	27	US-09-791-537-21879 Sequence 21879, A
30	542.5	54.5	199	31	US-10-152-300-2 Sequence 2, Appli
31	542.5	54.5	199	38	US-10-846-123-2 Sequence 2, Appli
32	542.5	54.5	200	27	US-09-791-537-6915 Sequence 6915, Ap
33	542.5	54.5	214	27	US-09-791-537-74454 Sequence 74454, A
34	542.5	54.5	214	27	US-09-791-537-127550 Sequence 127550, A
35	542.5	54.5	214	27	US-09-791-537-127562 Sequence 127562, A
36	542	54.4	214	27	US-09-791-537-17342 Sequence 17342, A
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38	542	54.4	214	27	US-09-791-537-128533 Sequence 128533, A
39	541.5	54.4	200	27	US-09-791-537-27160 Sequence 27160, A
40	541.5	54.4	214	27	US-09-791-537-127548 Sequence 127548, A
41	541.5	54.4	214	27	US-09-791-537-127555 Sequence 127555, A
42	541.5	54.4	214	27	US-09-791-537-127565 Sequence 127565, A
43	541	54.3	214	27	US-09-791-537-17359 Sequence 17359, A
44	541	54.3	214	27	US-09-791-537-17382 Sequence 17382, A
45	540	54.2	214	27	US-09-791-537-17385 Sequence 17385, A

ALIGNMENTS

RESULT 1

US-08-817-997-2
; Sequence 2, Application US/08817997
; GENERAL INFORMATION:
; APPLICANT: Sandal, Thomas

```
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Kofod, Lene V.
; TITLE OF INVENTION: An Enzyme With Lipolytic
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Novo Nordisk Of North America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,997
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4316.204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-878-9652
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 246 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-817-997-2

Query Match      100.0%; Score 996; DB 18; Length 246;
Best Local Similarity 100.0%; Pred. No. 1.7e-84;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
DB 36 OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 95
QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
DB 96 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 155
QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
DB 156 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 215
QY 181 RGEAARFLDRIRA 194
DB 216 RGEAARFLDRIRA 229

RESULT 2
US-10-152-300-1
; SEQUENCE 1, Application US/10152300
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Lund, Henrik
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Sticksies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/152,300
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Humicola insolens
; ORGANISM: Humicola insolens
US-10-846-123-1
Query Match      99.5%; Score 991; DB 38; Length 194;
Best Local Similarity 99.5%; Pred. No. 3.4e-84;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
DB 1 OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
DB 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
DB 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
QY 181 RGEAARFLDRIRA 194
DB 181 RGEAARFLDRIRA 194

RESULT 3
US-10-846-123-1
; SEQUENCE 1, Application US/10846123
; GENERAL INFORMATION:
; APPLICANT: Borch, Kim
; APPLICANT: Lund, Henrik
; APPLICANT: Sharyo, Masaki
; APPLICANT: Sakaguchi, Hiromichi
; APPLICANT: Pedersen, Hanne
; APPLICANT: Fitzhenry, James
; TITLE OF INVENTION: Use of Lipolytic Enzymes for Sticksies Control
; FILE REFERENCE: 10142
; CURRENT APPLICATION NUMBER: US/10/846,123
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US/10/152,300
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Humicola insolens
; ORGANISM: Humicola insolens
US-10-846-123-1
Query Match      99.5%; Score 991; DB 38; Length 194;
Best Local Similarity 99.5%; Pred. No. 3.4e-84;
Matches 193; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
DB 1 OLGAIENGLESGSANACPDAILIFARGSTPEGNMGITVGPALANGLESHERINWIQGVGG 60
QY 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
DB 61 PYDAALATNPLPRGTSQANIDEGKRLFALANQKCPNTPVAVAGYSQGAALIAAAVSELG 120
QY 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
DB 121 AVKEQVKGVALFGYTONLQNRGGIANYPRRTKVFNCVGDVAVCTGTLIITPAHLSYTTIEA 180
QY 181 RGEAARFLDRIRA 194
DB 181 RGEAARFLDRIRA 194
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RESULT 4
US-09-791-537-26059
; Sequence 26059, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26059
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Alternaria brassicicola
US-09-791-537-26059

Query Match 59.8%; Score 596; DB 27; Length 209;
Best Local Similarity 60.3%; Pred. No. 5.1e-47;
Matches 117; Conservative 22; Mismatches 53; Indels 2; Gaps 1;
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DB 13 QASTTRNELETSSDACPRITIFARGSTPEAGNMGALVGPFTANALESAYGASNVWQGV 72
QY 59 GGPYDAALATNPLPRTGTSQANIDEGKRLFALANQKCPNTPVAVGGYSGQAALIAAAVSEL 118
DB 73 GGPYTAGLVENALPAGTSQAAREAQRLFNLAASKCPNTPITAGGYSQGAAMVNSAIPGL 132
QY 119 SGAVKEOVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLLITPAHLSTYIE 178
DB 133 SRAVQDIKGVVLFGYTKLQNRGRIPDPFTKTEVCYNASDAVCFGLTLLPAHLFLYTYE 192
QY 179 EARGEAAFLDRRI 192
DB 193 EAAVQAPFLRAQI 206

RESULT 5
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; Sequence 32037, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32037
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Pyricularia grisea
US-09-791-537-32037

Query Match 59.6%; Score 593.5; DB 27; Length 228;
Best Local Similarity 59.5%; Pred. No. 9.9e-47;
Matches 116; Conservative 27; Mismatches 51; Indels 1; Gaps 1;
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DB 93 DPYDAALSPNPLPAGTITQGAIDEAKRMFTLANTKCPNAAVAVGGYSGQTAVMFAVSEMP 152

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DB 153 AAVQDIKGVVLFGYTKLQNRGRIPDPFTKTEVCYNASDAVCFGLTLLPAHLFLYTYE 212
QY 180 ARGEAAARFLDRIRA 194
DB 213 SSIAAPNWLIRQIRA 227

RESULT 6

US-08-171-805-59
; Sequence 59, Application US/08171805
; GENERAL INFORMATION:
; APPLICANT: EGMOND, Maarten Robert
; APPLICANT: VAN DER HUIDEN, Hendrikus Theodorus W.M.
; APPLICANT: MUSTERS, Wouter
; APPLICANT: PETERS, Hans
; APPLICANT: VERRIPS, Cornelis Theodorus
; APPLICANT: DE Vlieg, Jakob
; TITLE OF INVENTION: MODIFIED LIPOLYTIC ENZYMES AND THEIR USE
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT DEPARTMENT UNILEVER UNITED STATES INC.
; STREET: 45 RIVER ROAD
; CITY: EDGEWATER
; STATE: N.J.
; COUNTRY: USA
; ZIP: 07020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,805
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Koatz, Ronald A.
; REGISTRATION NUMBER: 31,774
; REFERENCE/DOCKET NUMBER: 93-0065-A-UNI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 943-7100
; TELEFAX: (201) 943-3661
; TELEX: 640 333 LEVER EDGE
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 196 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-171-805-59

Query Match 58.0%; Score 578; DB 11; Length 196;
Best Local Similarity 57.9%; Pred. No. 2.3e-45;
Matches 113; Conservative 28; Mismatches 52; Indels 2; Gaps 1;
QY 2 LGAIENGLESANACPDAILIFARGSTPEGNMGITVGPALANGLESHI--RNIWQGVG 59
DB 1 LNSVRNDLISGNAACPSVILIFARASGEVGNMGLSAGTNVASRLERERENDIWWQGVG 60
QY 60 GPYDAALATNPLPRTGTSQANIDEGKRLFALANQKCPNTPVAVGGYSGQAALIAAAVSEL 119
DB 61 DPYDAALSPNPLPAGTITQGAIDEAKRMFTLANTKCPNAAVAVGGYSGQTAVMFAVSEMP 120
QY 120 GAVKEOVKGVALFGYTONLQNRGGIANYPRTKVFNCVGDVAVCTGTLLITPAHLSTYIE 179
DB 121 AAVQDIKGVVLFGYTKLQNRGRIPDPFTKTEVCYNASDAVCFGLTLLPAHLFLYTYE 180
QY 180 ARGEAAARFLDRIRA 194

```
Db      181 SSIAAPNWLIRQIRA 195

RESULT 7
US-08-551-983-64
; Sequence 64, Application US/08551983
; GENERAL INFORMATION:
; APPLICANT: EGMOND, Maarten Robert
; APPLICANT: VAN DER HIJDEN, Hendrikus Theodorus W.M.
; APPLICANT: MUSTERS, Wouter
; APPLICANT: PETERS, Hans
; APPLICANT: VERRIPS, Cornelis Theodorus
; APPLICANT: DE Vlieg, Jakob
; TITLE OF INVENTION: MODIFIED LIPOLYTIC ENZYMES AND THEIR USE
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT DEPARTMENT UNILEVER UNITED STATES INC.
; STREET: 45 RIVER ROAD
; CITY: EDGEWATER
; STATE: N.J.
; COUNTRY: USA
; ZIP: 07020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/551,983
; FILING DATE: 17-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/169,803
; FILING DATE: 17-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Koatz, Ronald A.
; REGISTRATION NUMBER: 31,774
; REFERENCE/DOCKET NUMBER: 93-0064-A-UNI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 943-7100
; TELEFAX: (201) 943-3661
; TELEX: 640 333 LEVER EDGE
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 196 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-551-983-64

Query Match      58.0%; Score 578; DB 15; Length 196;
Best Local Similarity 57.9%; Pred. No. 2.3e-45;
Matches 113; Conservative 28; Mismatches 52; Indels 2; Gaps 1;

Qy      2 LGAIENLSEGSANACPDAILIFARGSTPEGNMGITVGPALANGLSHI--RNIIWQGVG 59
Db      1 LNSVRNDLISGNAACPSVILIFARASGEVGNMGLSAGTNVASRLERFGRNDIWOQGVG 60
Qy      60 GPYDAALATNLFPRGTGTSQANIDEGKRLFALANOKCPNTFPVAGYSQGAALIAAAVSELS 119
Db      61 DPYDAALSNFLPAGTITQGAIDSAKGMFTLTANTKCPNAAVAGYSQGTAVMFAVNSEMP 120
Qy      120 GAVKEQKGVVALFGYTNQNLQNRGGIANYPRRTKVFNCNVGDVACTGTLLITPAHLSYTIIE 179
Db      121 AAVQDIKGVWLEGYTKNLQNRGRIPDPFTEKTEVCYNASDAVCFGLFLPAHFLYTTIE 180
Qy      180 ARGEAAARFLRDTRI 194
Db      181 SSIAAPNWLIRQIRA 195

RESULT 8
US-08-171-805-57
; Sequence 57, Application US/08171805
; GENERAL INFORMATION:
; APPLICANT: EGMOND, Maarten Robert
; APPLICANT: VAN DER HIJDEN, Hendrikus Theodorus W.M.
; APPLICANT: MUSTERS, Wouter
; APPLICANT: PETERS, Hans
; APPLICANT: VERRIPS, Cornelis Theodorus
; APPLICANT: DE Vlieg, Jakob
; TITLE OF INVENTION: MODIFIED LIPOLYTIC ENZYMES AND THEIR USE
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT DEPARTMENT UNILEVER UNITED STATES INC.
; STREET: 45 RIVER ROAD
; CITY: EDGEWATER
; STATE: N.J.
; COUNTRY: USA
; ZIP: 07020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,805
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Koatz, Ronald A.
; REGISTRATION NUMBER: 31,774
; REFERENCE/DOCKET NUMBER: 93-0065-A-UNI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 943-7100
; TELEFAX: (201) 943-3661
; TELEX: 640 333 LEVER EDGE
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-171-805-57

Query Match      57.8%; Score 576; DB 11; Length 194;
Best Local Similarity 58.5%; Pred. No. 3.5e-45;
Matches 110; Conservative 28; Mismatches 48; Indels 2; Gaps 1;

Qy      7 NGLSEGSANACPDAILIFARGSTPEGNMGITVGPALANGLS--HIRNIWQGVGYPDA 64
Db      6 NELETSSSACPKVIYIFARASTPEGNMGISAGTIVADALERIYCANNVWQGVGYPILA 65
Qy      65 ALATNLFPRGTGTSQANIDEGKRLFALANOKCPNTFPVAGYSQGAALIAAAVSELSGAVKE 124
Db      66 DLASNFLPDGTSSAAINEARLFTLANTKCPNAAIVSGYSQGTAVMAGSISGLSTTIKN 125
Qy      125 QVKGVALFGYTNQNLQNRGGIANYPRRTKVFNCNVGDVACTGTLLITPAHLSYTIIEARGEA 184
Db      126 QIKGVWLFYGYTKNLQNLGRIPNFTSKTEVCYDIADAVCYGTLFILPAHFLYQTDAAVAA 185
Qy      185 ARFLRDRI 192
Db      186 PRFLQARI 193

RESULT 9
US-08-551-983-62
; Sequence 62, Application US/08551983
; GENERAL INFORMATION:
; APPLICANT: EGMOND, Maarten Robert
```


FILING DATE: 17-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Koatz, Ronald A.
REGISTRATION NUMBER: 31,774
REFERENCE/DOCKET NUMBER: 93-0064-A-UNI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 943-7100
TELEFAX: (201) 943-3661
TELEX: 640 333 LEVER EDGE
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 194 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-551-983-63

Query Match
Best Local Similarity 56.3%; Score 561; DB 15; Length 194;
Matches 108; Conservative 27; Mismatches 51; Indels 2; Gaps 1;

QY 7 NGLSGSANACPDAILIFARGSTPGNMGITVGPALANGLESH--IRNIWQVGGPYDA 64
DB 6 NELESGSSNCPKVIYIFARASTPGNMGISAGPIVADALESRYGASQVWVQVGGPYSA 65
QY 65 ALATNPLPGTQANIDEGRKLFALANQKCPNTPVWAGGYSQGAALIAAAVSELSGAVKE 124
DB 66 DLASNFIPEGTSRVAINAKRLFTLANTKCPNSAVVAGGYSQGTAVWASSISELSSTION 125
QY 125 QVKGVALFGYTONLQNRGGIANYPRERTKVCNVGDVAVCTGTLIITPAHLSYTIARGEA 184
DB 126 QIKGVVLSAITKQLNQLRIPNFTSKTEVYCALADAVCVGTFLFPAHFLYQADAATSA 185
QY 185 ARFLRDRI 192
DB 186 PRELAARI 193

RESULT 15
US-09-791-537-17346
Sequence 17346, Application US/09791537
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 17346
LENGTH: 214
TYPE: PRT
ORGANISM: pdb 1CUWA
US-09-791-537-17346

Query Match
Best Local Similarity 55.6%; Score 554; DB 27; Length 214;
Matches 110; Conservative 31; Mismatches 52; Indels 4; Gaps 3;

QY 1 QLG-ATENGLEGSANACPDAILIFARGSTPGNMGITVGPALANGLESHI--RNIWIOG 57
DB 14 QLGRTTRDDLINGSASCADVIFARYGSTETGNLG-TLGPSTASNLESFAGKDGWVIOG 72
QY 58 VGGPYDAALATNPLPGTQANIDEGRKLFALANQKCPNTPVWAGGYSQGAALIAAVSE 117
DB 73 VGGAYRATLADNPLPRGTSAAIREMLGLFQQANTKCPDATLIAGGYSQGAALAAASIED 132
QY 118 LSGAVKEQVKGVALFGYTONLQNRGGIANYPRERTKVCNVGDVAVCTGTLIITPAHLSYT 177

Db 133 LDSAIRDKIAGTVLFGYTKNLQNRGRIPNYPADRTKVCNCTGDLVCTGSLIILAPHFAYG 192
QY 178 IEARGEAAARFLDRIRA 194
DB 193 PDARGPAPEFLIEKVRA 209

Search completed: February 4, 2006, 05:07:58
Job time : 601 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 4, 2006, 04:58:04 ; Search time 35 Seconds

(without alignments)

385.289 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGATENGLESANACPDPA.....SVTIARGEARFLDRIRA 194

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 259879 seqs, 69510979 residues

Total number of hits satisfying chosen parameters: 259879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New.*

1: /cgn2_6/prodata/2/paa/pct/US06_NEW_COMB.pep.*
2: /cgn2_6/prodata/2/paa/pct/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/2/paa/pct/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/2/paa/pct/US08_NEW_COMB.pep.*
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6: /cgn2_6/prodata/2/paa/pct/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/2/paa/pct/US11_NEW_COMB.pep.*
8: /cgn2_6/prodata/2/paa/pct/US60_NEW_COMB.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	242.5	24.3	686	1	PCT-US06-00964-8187
2	242.5	24.3	686	7	US-11-330-403-8187
3	234.5	23.5	1003	1	PCT-US06-00964-10079
4	234.5	23.5	1003	7	US-11-330-403-10079
5	88	8.8	1356	8	US-60-752-355-22033
6	87	8.7	1356	8	US-60-752-355-5682
7	87	8.7	1356	8	US-60-752-355-5686
8	87	8.7	1356	8	US-60-752-355-5687
9	86.5	8.7	649	7	US-11-311-940-9837
10	86	8.6	1331	7	US-11-311-940-5856
11	85	8.5	7510	8	US-60-752-355-12835
12	84.5	8.5	628	1	PCT-US06-00964-1798
13	84.5	8.5	628	7	US-11-330-403-1798
14	84.5	8.5	772	8	US-60-752-355-22380
15	84.5	8.5	1376	8	US-60-752-355-5711
16	84.5	8.5	2082	1	PCT-US06-00964-9531
17	84.5	8.5	2082	7	US-11-330-403-9531
18	82	8.2	1424	7	US-11-311-940-8349
19	80	8.0	440	7	US-11-311-940-7587
20	80	8.0	515	1	PCT-US06-00964-18288
21	80	8.0	515	7	US-11-330-403-18288
22	80	8.0	653	6	US-10-953-349-33827
23	80	8.0	784	6	US-10-953-349-33826
24	80	8.0	841	6	US-10-953-349-33825
25	79.5	8.0	545	8	US-60-752-355-48339

26	79	7.9	296	7	US-11-246-957-20	Sequence 20, Appl
27	79	7.9	298	8	US-60-752-355-47282	Sequence 47282, A
28	79	7.9	311	8	US-60-752-355-21315	Sequence 21315, A
29	79	7.9	441	7	US-11-311-940-5952	Sequence 5952, Ap
30	79	7.9	442	7	US-11-311-940-4963	Sequence 4963, Ap
31	79	7.9	462	7	US-11-311-940-5687	Sequence 5687, Ap
32	78.5	7.9	303	6	US-10-953-349-1993	Sequence 1993, Ap
33	78.5	7.9	377	6	US-10-953-349-1992	Sequence 1992, Ap
34	78.5	7.9	382	6	US-10-953-349-1991	Sequence 1991, Ap
35	78.5	7.9	411	8	US-60-752-355-36639	Sequence 36639, A
36	78.5	7.9	1536	1	PCT-US06-00964-1325	Sequence 1325, Ap
37	78.5	7.9	1536	7	US-11-330-403-1325	Sequence 1325, Ap
38	78	7.8	297	7	US-11-246-957-14	Sequence 14, Appl
39	78	7.8	424	1	PCT-US06-00964-6292	Sequence 6292, Ap
40	78	7.8	424	1	PCT-US06-00964-14726	Sequence 14726, A
41	78	7.8	424	7	US-11-330-403-6292	Sequence 6292, A
42	78	7.8	424	7	US-11-330-403-14726	Sequence 14726, A
43	78	7.8	470	8	US-60-752-355-4514	Sequence 4514, Ap
44	77.5	7.8	385	8	US-60-752-355-46534	Sequence 46534, A
45	77.5	7.8	497	1	PCT-US06-00964-9830	Sequence 9830, Ap

ALIGNMENTS

RESULT 1

PCT-US06-00964-8187
; Sequence 8187, Application PC/TUS0600964
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: PCT/US06/00964
; CURRENT FILING DATE: 2006-01-23
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 8187
; LENGTH: 686
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
PCT-US06-00964-8187

Query Match 24.3%; Score 242.5; DB 1; Length 686;

Best Local Similarity 37.4%; Pred. No. 1.2e-13;

Matches 76; Conservative 25; Mismatches 67; Indels 35; Gaps 10;

Qy	2	LGATENG	-----ESGSA-----	NACPDAILIFARGSTPCNMGITVGPALANGLESHI	50
Db	497	LGKLPALGKRSRSGSTNSDVTNSGCKELTFIARGTTEIGNMGTVVGPVKGEALKSUT	556		
Qy	51	RN-IWIOGVGPDYDAALATNPLPRGTSQANTIDEGKRLPAL---	ANQKCPNTPVAVGYSQ	106	
Db	557	GNKAAIOGVDPADAA-----	GNAALGGSGGPKMASLVETALKQCPDTKIVLGGYSQ	608	
Qy	107	GAALIAAANSELGAVKEQKVGVALPGYTONLQNRGGIANVPRRTKVPNCNVGDVAVC-TG	165		
Db	609	GAMVHVNAASKLSGG---QVVGAVTFGDPFKSQKPDNI-----	DQFKTFCASGDPVCLNG	660	
Qy	166	TLITPAHLSTVTEARGEARFL	188		
Db	661	ANVM--AHLSTYGNDAQ-TAAQFL	680		

RESULT 2

US-11-330-403-8187
; Sequence 8187, Application US/11330403
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 8187


```
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Podospora anserina
US-60-752-355-5682

Query Match      8.7%; Score 87; DB 8; Length 1356;
Best Local Similarity 23.2%; Pred. No. 23;
Matches 38; Conservative 23; Mismatches 77; Indels 26; Gaps 5;

Qy   39 GPALANGLESHIRNIW-----IQGVGGPYDAALATNPLPRG--TSQANIDEGKRLFAL 89
Db   1105 GQRVASSGDHDTIKIWDAAAGTCTQTLEGHGDSVWSVAFPDQGRVASSGIDGTIKIWD 1164
Qy   90 ANQKCPNTPVVAGYSOGAALIAAAVSELSGAVKEQVK--GVALFGYTQNLRGG---- 143
Db   1165 ASGTCTQTLEHGCGVHVSVAFSPDQGRVASSGIDGTIKIWDAAAGTCTQTLEHGCGVHS 1224
Qy   144 -----TANYPRETKVFCNVGDVACTGTGLII--TPAHLVS 176
Db   1225 VAFSPDQGRVASSGSDNTIKIWDATASGTCQTTLNVGSTATCLSF 1268

RESULT 7
US-60-752-355-5686
; Sequence 5686, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)B
; CURRENT APPLICATION NUMBER: US/60752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5686
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Podospora anserina
US-60-752-355-5686

Query Match      8.7%; Score 87; DB 8; Length 1356;
Best Local Similarity 23.2%; Pred. No. 23;
Matches 38; Conservative 23; Mismatches 77; Indels 26; Gaps 5;

Qy   39 GPALANGLESHIRNIW-----IQGVGGPYDAALATNPLPRG--TSQANIDEGKRLFAL 89
Db   1105 GQRVASSGDHDTIKIWDAAAGTCTQTLEGHGDSVWSVAFPDQGRVASSGIDGTIKIWD 1164
Qy   90 ANQKCPNTPVVAGYSOGAALIAAAVSELSGAVKEQVK--GVALFGYTQNLRGG---- 143
Db   1165 ASGTCTQTLEHGCGVHVSVAFSPDQGRVASSGIDGTIKIWDAAAGTCTQTLEHGCGVHS 1224
Qy   144 -----TANYPRETKVFCNVGDVACTGTGLII--TPAHLVS 176
Db   1225 VAFSPDQGRVASSGSDNTIKIWDATASGTCQTTLNVGSTATCLSF 1268

RESULT 8
US-60-752-355-5687
; Sequence 5687, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)B
; CURRENT APPLICATION NUMBER: US/60752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5687
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Podospora anserina
US-60-752-355-5687
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Db 329 NTWDTLSAFADDEVTRVAREVGTGRGLGQANVPNVAGTWKDLTDNVSMANLNTQVRN 388 :||| : :||
Qy 53 IWIQGVGPGYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPV-VAGGYSQGAALI 111 :||| : :||
Db 389 I-----ALVTTAVARGDLKKIDVDARGEILELKTINTWVDLSAFADDEVTRV 437 :||| : :||
Qy 112 AAAY-----SELGAVKQVGVGVALFGYTONL-QNRGGIANYPRTKVFNCVGDVCTGTL 167 :||| : :||
Db 438 AREVTEGRGG--QAEVEGVS--GTWKRLTENVNELAGNLTRQVRAEVTSAVAGDL 493 :||| : :||
Qy 168 IITPAHLSYTIAREGEAARFLDRRA 194 :||| : :||
Db 494 T-----RSVTVEASGEVAE-LGDNINA 514 :||| : :||

RESULT 11
US-60-752-355-12835
; Sequence 12835, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)B
; CURRENT APPLICATION NUMBER: US/60/752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12835
; LENGTH: 7510
; TYPE: PRT
; ORGANISM: Streptomyces aizunensis
US-60-752-355-12835

Query Match 8.5%; Score 85; DB 8; Length 7510;
Best Local Similarity 24.2%; Pred. No. 3.6e+02;
Matches 54; Conservative 30; Mismatches 85; Indels 54; Gaps 11;
Qy 1 OLGAITENGLE-----SGSANACPDAILIFARGSTEGPNCMGITVGPALANGL-----ESHI 50 :||| : :||
Db 1964 RLPAPVEGLEGLGTGTAGSVASGRISYTFGLEGP---AVTVDTCSSSLVALHLAAQAL 2020 :||| : :||
Qy 51 RNIWIQGVGPGYDAALATNPLPRGTSQANIDEGKRLFALANOKCPNTPVAG--GYSQGA 108 :||| : :||
Db 2021 RN-----GECDMALAGGVTVMTPTDFIDFSRQRLSGNGRCKSFSADADGTGWAGA 2073 :||| : :||
Qy 109 ALIAAAVSELSCA-----VKEQVGVGVALFGYTONLQNRGGIAN-----YPRRTK 153 :||| : :||
Db 2074 GMI--LVERLSDARNHGQVLAVVRGTAV-----NODGASNGLTAPNPSQQRVIRQ 2123 :||| : :||
Qy 154 VFCNVGDVCTGTLITPAH-----LSYTIAREGEAARFLDRR 191 :||| : :||
Db 2124 ALANAG--LTTAEVDVVEAHGTGTLGDPIEAQALLATYQQR 2164 :||| : :||

RESULT 12
PCT-US06-00964-1798
; Sequence 1798, Application PC/TUS0600964
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: PCT/US06/00964
; CURRENT FILING DATE: 2006-01-23
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 1798
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Glycine max
PCT-US06-00964-1798

Query Match 8.5%; Score 84.5; DB 1; Length 628;
Best Local Similarity 18.8%; Pred. No. 14;
Matches 37; Conservative 41; Mismatches 66; Indels 53; Gaps 7;

Qy 13 SANACPDAILIFARGSTEGPNCMGITVGPALANGLSHIRNIWIQGVGPGYDAALATNPLP 72 :||| : :||
Db 427 SSDVILDPLLSLRKGLAVPGDVKVSVDNDIIVKVAALRNV-----P 468 :||| : :||
Qy 73 RGTQSANIDEGKRL-----FALANOKCPNTPVAGGYSQGAALIAAAVSELSGAVKE 124 :||| : :||
Db 469 ENAYVNVKEGVVVLNDSIDICIAVATEKGLMTPIIKNADOKTISAISSSEVKELAAKARA 528 :||| : :||
Qy 125 -QVKGVALFGYTONLQNRGGIANYPRTKVFNCVGD-----AVCTGTLLIITP----- 171 :||| : :||
Db 529 GKLPHEFGGTFISINLG---MFPVDK---FCAIINPPQACILAVGRGNKVVEPVIGTD 582 :||| : :||
Qy 172 -----AHLSTYIEA 180 :||| : :||
Db 583 GIEKPSIATKLSLTLSA 599 :||| : :||

RESULT 13
US-11-330-403-1798
; Sequence 1798, Application US/11330403
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)B
; CURRENT APPLICATION NUMBER: US/11/330,403
; CURRENT FILING DATE: 2006-01-12
; NUMBER OF SEQ ID NOS: 19250
; SEQ ID NO 1798
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Glycine max
US-11-330-403-1798

Query Match 8.5%; Score 84.5; DB 7; Length 628;
Best Local Similarity 18.8%; Pred. No. 14;
Matches 37; Conservative 41; Mismatches 66; Indels 53; Gaps 7;
Qy 13 SANACPDAILIFARGSTEGPNCMGITVGPALANGLSHIRNIWIQGVGPGYDAALATNPLP 72 :||| : :||
Db 427 SSDVILDPLLSLRKGLAVPGDVKVSVDNDIIVKVAALRNV-----P 468 :||| : :||
Qy 73 RGTQSANIDEGKRL-----FALANOKCPNTPVAGGYSQGAALIAAAVSELSGAVKE 124 :||| : :||
Db 469 ENAYVNVKEGVVVLNDSIDICIAVATEKGLMTPIIKNADOKTISAISSSEVKELAAKARA 528 :||| : :||
Qy 125 -QVKGVALFGYTONLQNRGGIANYPRTKVFNCVGD-----AVCTGTLLIITP----- 171 :||| : :||
Db 529 GKLPHEFGGTFISINLG---MFPVDK---FCAIINPPQACILAVGRGNKVVEPVIGTD 582 :||| : :||
Qy 172 -----AHLSTYIEA 180 :||| : :||
Db 583 GIEKPSIATKLSLTLSA 599 :||| : :||

RESULT 14
US-60-752-355-22380
; Sequence 22380, Application US/60752355
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark et al.
; TITLE OF INVENTION: Transgenic plants with enhanced agronomic traits
; FILE REFERENCE: 38-21(53720)B
; CURRENT APPLICATION NUMBER: US/60/752,355
; CURRENT FILING DATE: 2005-12-21
; NUMBER OF SEQ ID NOS: 52803
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22380
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Magnetospirillum gryphiswaldense
US-60-752-355-22380

Query Match 8.5%; Score 84.5; DB 8; Length 772;

GenCore version 5.1.7
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OM protein - nucleic search, (using frame plus_p2n model)

Run on: February 4, 2006, 21:44:24 ; Search time 4847 Seconds
(without alignments)
2275.145 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGATENGLESANACPD.....SYTIEARGEARFLDRIRA 194

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-YGAPOPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.hg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991	99.5	994	6	AR050618 Sequence
2	552	55.4	1545	15	ABU03393
3	546	54.8	718	6	A36991 Sequence 42

4	546	54.8	718	6	A39199	A39199 Sequence 47
5	546	54.8	718	6	A39258	A39258 Sequence 42
6	546	54.8	1121	6	A00975	A00975 F.solani mR
7	545	54.7	883	15	FSOCUT	K02640 F.solani pi
8	544.5	54.7	1749	15	COGCUA	M21443 C.gloeospor
9	539.5	54.2	5768	15	AF444194	AF444194 Glomerell
10	531.5	53.4	3938	15	FSU63335	U63335 Nectria ipo
11	531	53.3	2557	15	COGCUA	M18033 C.capsici c
12	519.5	52.2	1735	15	AF417004	AF417004 Nectria h
13	519.5	52.2	2769	15	FSOCUT	M29759 F.solani cu
14	518.5	52.0	1662	15	ARCUT	X65628 A.rabiei c
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16	517	51.9	2049	15	MGCUT1	X61500 M.grisea cu
17	506	50.8	789	6	CO788695	CO788695 Sequence
18	500.5	50.3	914	6	AR195188	AR195188 Sequence
19	499.5	50.2	999	6	AR195190	AR195190 Sequence
20	482	48.4	869	6	AR195189	AR195189 Sequence
21	430	43.2	2371	6	CO788694	CO788694 Sequence
22	388.5	39.0	1350	15	ASNC	D38311 Aspergillus
23	262	26.3	280	6	A36990	A36990 Sequence 41
24	262	26.3	280	6	A39198	A39198 Sequence 46
25	262	26.3	280	6	A39257	A39257 Sequence 41
26	260	26.1	768	6	AX767352	AX767352 Sequence
27	260	26.1	798	6	BD184000	BD184000 Microorga
28	260	26.1	798	6	AR300500	AR300500 Sequence
29	260	26.1	798	6	AR594235	AR594235 Sequence
30	260	26.1	798	6	AR613466	AR613466 Sequence
31	260	26.1	798	6	AR647284	AR647284 Sequence
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33	260	26.1	798	6	BD004787	BD004787 Esterase
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35	212	21.3	246	6	A36975	A36975 Sequence 26
36	212	21.3	246	6	A39183	A39183 Sequence 31
37	212	21.3	246	6	A39242	A39242 Sequence 26
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40	193	19.4	289308	1	AE017242	AE017242 Mycobacte
41	192	19.3	1025	15	AB039325	AB039325 Aspergill
42	189.5	19.0	651	6	AR456004	AR456004 Sequence
43	189.5	19.0	654	6	BD273847	BD273847 Sequences
44	189.5	19.0	654	6	AX005139	AX005139 Sequences
45	189.5	19.0	720	6	BD273848	BD273848 Sequences

ALIGNMENTS

RESULT 1	AR050618	Sequence 1 from patent US 5827719.	994 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR050618					
DEFINITION	Sequence 1 from patent US 5827719.					
ACCESSION	AR050618					
VERSION	AR050618.1	GI:5973343				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 994)					
AUTHORS	Sandal, T., Kauppinen, S. and Kofod, L. Venke.					
TITLE	Enzyme with lipolytic activity					
JOURNAL	Patent: US 5827719-A 1 27-OCT-1998;					
FEATURES	Location/Qualifiers					
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	/organism="unknown"					
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Alignment Scores:						
Pred. No.:	1.12e-71	Length:	994			
Score:	991.00	Matches:	193			
Percent Similarity:	99.5%	Conservative:	0			
Best Local Similarity:	99.5%	Mismatches:	1			
Query Match:	99.5%	Indels:	0			
DB:	6	Gaps:	0			


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QY 1 GlnLeuGlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAla 20
Db 148 CAGCTGGAGCCATCGAGAACGGCTTGAGAGCGGAGCCCAACGCTCGCCGAGCGC 207
QY 21 IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyPro 40
Db 208 ATCTGTATCTTTGCTCGCGCTCGACCGAGCGAGGCAACATGGGCATCACCGTCGCGCT 267
QY 41 AlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrrIleGlnGlyValGlyGly 60
Db 268 GCTCTCGCAACCGGCTTGAGTCCACATCCGGAACATCTGGATCCAGGCGGTGCGCGC 327
QY 61 ProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle 80
Db 328 CTTTACGAGCGCGCTGGCCACCACTTCTGCGCGGGGNCCTCGAGCGGCAACATC 397
QY 81 AspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValVal 100
Db 388 GACGAGGGCAACGGCTGTTTGGCTGGCCAAACCAAAAGTGCCCAACACGCGCGTCTC 447
QY 101 AlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlnLeuSerGly 120
Db 448 GCCGGCGGGTACAGCGAGCGCGCGCTCATGCTGCGCGCGCTCAGCGAGCTCAGCGC 507
QY 121 AlaValGluGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn 140
Db 508 GCCGTCAAGGACAGGTCAAGGCGCTGCGCCCTCTTCGGATACCCCAAACTCCAGAAC 567
QY 141 ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp 160
Db 568 CGTGGCGGCATCCCAACTACCGCGCGAGCGCACCAAGGTGTTCTGCAAGGTTGCGAC 627
QY 161 AlaValCysThrGlyThrIleuIleThrProAlaHisLeuSerTyrThrIleGluAla 180
Db 628 GCGGTCTGACCGGACGCTCATCATCACCCTGCGCGCATCTGTGTACAGCATCGAGCG 687
QY 181 ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 688 CGCGGTGAGCGCGAGGTCTTCTGCGGGATCGCATCCGTCT 729

RESULT 2
ABU03393
LOCUS
DEFINITION Alternaria brassicicola cutinase (cutab1) gene, complete cds.
ACCESSION U03393
VERSION U03393.1 GI:416217
KEYWORDS
SOURCE
  Alternaria brassicicola
  Alternaria brassicicola
  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
  Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.
  Yao,C. and Koeller,W.
  Cloning and characterization of a cutinase gene from Alternaria
  brassicicola
  Physiol. Mol. Plant Pathol.
  2 (bases 1 to 1545)
  Yao,C.
  Direct Submission
  Submitted (09-NOV-1993) Chenglin Yao, Plant Pathology, Cornell
  University, Geneva, NY 14456, USA
  Location/Qualifiers
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     /mol_type="unassigned DNA"
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     550..1235
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FEATURES
source
gene
CDS
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RESULT 3
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LOCUS       A36991                718 bp    DNA                linear    PAT 05-MAR-1997
DEFINITION   Sequence 42 from Patent WO9403578.
ACCESSION   A36991
VERSION     A36991.1  GI:2294185
KEYWORDS
SOURCE      unidentified
            unclassified sequences.
            1 (bases 1 to 718)
REFERENCE   1  (bases 1 to 718)
AUTHORS     Hijden,H.T., Marugg,J.D., Warr,J.F., Klugkist,J., Musters,W. and
            Hondmann,D.H.
TITLE       ENZYMATIC DETERGENT COMPOSITIONS
JOURNAL
COMMENT     Patent: WO 9403578-A 42 17-FEB-1994;
            UNILEVER PLC (GB)
            Other publication CZ 9500242 951018
            Other publication CN 1088256 940622
            Other publication PL 307269 950515
            Other publication CA 2141559 940217
            Other publication AU 4700793 940303
            Other publication ZA 9305530 950130
            Other publication JP 8502084T 960305.
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Alignment Scores:
Pred. No.:      1.36e-35      Length:      718
Score:          546.00      Matches:    108
Percent Similarity: 71.1%      Conservative: 32
Best Local Similarity: 54.8%      Mismatches: 53
Query Match:    54.8%      Indels:    4
DB:              6      Gaps:      3

US-08-817-997-2_COPY_36_229 (1-194) x A36991 (1-718)
QY      1 GlnLeuGly----AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
DB      103 CAGCTTGGTAGACAACACTCGCGAGCTCTGATCAACGGCAATAGCGCTTCTCGCGCGAT 162
QY      20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
DB      163 GTCATCTTCAATTTATGCTCAGGTTCAACAGAGACGGGCACTTGGGA---ACTCTCGGG 219
QY      40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
DB      220 CCAGCATTCCTCCCAACCTTGAGTCGCTCGGCAAGGACGGTGTCTGGATTACGGGC 279
QY      58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
DB      280 GTTGGCGGTGCTTACCGAGCACCTTAGAGACAATGCTCTCCCGCGGGAACTCTTAGC 339
QY      78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
DB      340 GCCGCAATCAGGAGATGCTAGCGCTTCTCCAGAGCCCAACACCAAGTCCCTCGACGCG 399
QY      98 ProValValAlaGlyTyrSerGlnGlyValAlaLeuIleAlaAlaValSerGlu 117
DB      400 ACTTTGATCGCGGTGGCTACACCGAGGTCGTGCACTTCAGCGCGTAGCATCGAGGAC 459
QY      118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
DB      460 CTCGACTCGGCCATTGCTGACAAGATCGCGGTACCGTTCTGTTTGGCTACCAACAAGAC 519
QY      138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
DB      520 CTACAGAAATCGCGCGCAATCCCAACTACCTCTCGCGCAGGACCAAGGTCCTTCGCAAT 579
QY      158 ValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThr 177
DB      590 ACAGGATCTCGTTTGTACTGTTGATGCTGTGCTGCACCTCATTGGCATATGGT 639
QY      178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
DB      640 CTTGATGCCGGGACCTGCCCTCAGTTCTCTCATCGAGAGGTTCCGGGT 690

RESULT 4
A39199
LOCUS       A39199                718 bp    DNA                linear    PAT 05-MAR-1997
DEFINITION   Sequence 47 from Patent WO9414963.
ACCESSION   A39199
VERSION     A39199.1  GI:2295568
KEYWORDS
SOURCE      unidentified
            unclassified sequences.
            1 (bases 1 to 718)
REFERENCE   1  (bases 1 to 718)
AUTHORS     Egmond,M.R., Van,D.H., Musters,W., Peters,H., Verrips,C.T. and
            De,V.J.
TITLE       MODIFIED CUTINASES, DNA, VECTOR AND HOST
JOURNAL
COMMENT     Patent: WO 9414963-A 47 07-JUL-1994;
            UNILEVER PLC (GB)
            Other publication SK 79595 951108
            Other publication PL 309388 951002
            Other publication CA 2150837 940707
            Other publication AU 5699994 940719
            Other publication CN 1090328 940803
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            Other publication ZA 9309415 950615.
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ORIGIN
Alignment Scores:
Pred. No.:      1.36e-35      Length:      718
Score:          546.00      Matches:    108
Percent Similarity: 71.1%      Conservative: 32
Best Local Similarity: 54.8%      Mismatches: 53
Query Match:    54.8%      Indels:    4
DB:              6      Gaps:      3

US-08-817-997-2_COPY_36_229 (1-194) x A39199 (1-718)
QY      1 GlnLeuGly----AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
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QY      20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
DB      163 GTCATCTTCAATTTATGCTCAGGTTCAACAGAGACGGGCACTTGGGA---ACTCTCGGG 219
QY      40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
DB      220 CCAGCATTCCTCCCAACCTTGAGTCGCTCGGCAAGGACGGTGTCTGGATTACGGGC 279
QY      58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
DB      280 GTTGGCGGTGCTTACCGAGCACCTTAGAGACAATGCTCTCCCGCGGGAACTCTTAGC 339
QY      78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
DB      340 GCCGCAATCAGGAGATGCTAGCGCTTCTCCAGAGCCCAACACCAAGTCCCTCGACGCG 399
QY      98 ProValValAlaGlyTyrSerGlnGlyValAlaLeuIleAlaAlaValSerGlu 117
DB      400 ACTTTGATCGCGGTGGCTACACCGAGGTCGTGCACTTCAGCGCGTAGCATCGAGGAC 459
QY      118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
DB      460 CTCGACTCGGCCATTGCTGACAAGATCGCGGTACCGTTCTGTTTGGCTACCAACAAGAC 519
QY      138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
DB      520 CTACAGAAATCGCGCGCAATCCCAACTACCTCTCGCGCAGGACCAAGGTCCTTCGCAAT 579
QY      158 ValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThr 177
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Db      460 CTCGACTCGGCCATTCTGTCACAGATCGCGGTACCGTTCTGTTCGGCTACACCAAGAAC 519
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Db      520 CTACAGATCGCGCGCGAATCCCACTACCTGCCGACAGGACCAAGGTCTTCTGCAAT 579
Qy      158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db      580 ACAGGAGATCTCGTTTGTACTGTAGTCTGATCGTTCGTCACCTCACTTGGCATATGGT 639
Qy      178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db      640 CCTGATGCCGGGACCTGCCCTGAGTTCTCTATCATCAGAAAGTTCCGGCT 690

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DEFINITION Sequence 42 from Patent WO9414964.
ACCESSION  A39258
VERSION    A39258.1  GI:2295623
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified sequences.
REFERENCE  1 (bases 1 to 718)
AUTHORS    Egmond,M.R., Van,D.H., Musters,W., Peters,H., Verrips,C.T. and
            De,V.J.
TITLE      MODIFIED CUTINASES, DNA, VECTOR AND HOST
JOURNAL    UNILEVER NV (NL)
COMMENT    Patent: WO 9414964-A 42 07-JUL-1994;
            Other publication CA 2151038 940707
            Other publication HU 71315 951128
            Other publication PL 309403 951002
            Other publication AU 5700094 940719
            Other publication SK 80295 951011
            Other publication CN 1090329 940803
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ORIGIN

Alignment Scores:
Pred. No.:          1.36e-35      Length:          718
Score:              546.00      Matches:         108
Percent Similarity: 71.1%      Conservative:    32
Best Local Similarity: 54.8%    Mismatches:     53
Query Match:        54.8%      Indels:          4
DB:                  6          Gaps:           3

US-08-817-997-2_COPY_36_229 (1-194) x A39258 (1-718)
Qy      1  GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db      103 CAGCTTGGTAGACAACATCGCGAGATCTATCAACGGCAATAGCGTCTCTCGCGCCGAT 162
Qy      20  AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
Db      163 GTCATCTTCAATTTATGCTCGAGGTTCAACAGACGGCGCACTTGGGA---ACTCTCGGG 219
Qy      40  ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
Db      220 CCCAGCATTCCTCCCACTTGTAGTCCGCTTCGGCAAGGACGGTGTCTGGATTGAGGC 279
Qy      58  ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
Db      280 GTTGGCGGTGCTACCGAGCCACCTAGGAGACAATGCTCTCCGCGGGGAACCTCTAGC 339
Qy      78  AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97

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Db      340 GCCCAATCAGGAGATGCTAGGCTCTTTCAGCAGGCGCAACACCAAGTGCCTGACGGC 399
Qy      98  ProValValaIleGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlu 117
Db      400 ACTTTGATCGCGGTGGCTACAGCAGGCTGCTGCACTTGCGCGCTAGCATCGAGGAC 459
Qy      118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db      460 CTCGACTCGGCATTCGTGACAAGATCGCGCTACCGTTCTGTTCGGCTACACCAAGAAC 519
Qy      138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
Db      520 CTACAGATCGCGCGCGAATCCCACTACCTGCCGACAGGACCAAGGTCTTCTGCAAT 579
Qy      158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db      580 ACAGGAGATCTCGTTTGTACTGTAGTCTGATCGTTCGTCACCTCACTTGGCATATGGT 639
Qy      178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db      640 CCTGATGCCGGGACCTGCCCTGAGTTCTCTATCATCAGAAAGTTCCGGCT 690

RESULT 6
LOCUS      A00975              1121 bp      RNA      linear      PAT 26-FEB-1993
DEFINITION F.solani mRNA for recombinant cutinase gene.
ACCESSION  A00975
VERSION    A00975.1  GI:14694
KEYWORDS   cutinase.
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1 (bases 1 to 1121)
AUTHORS    De,Geus.
TITLE      CUTINASE
JOURNAL    Patent: WO 9009446-A 1 23-AUG-1990;
            Location/Qualifiers
FEATURES             Location/Qualifiers
     source           1..1121
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     269..961
                     /codon_start=1
                     /transl_table=11
                     /product="cutinase-precursor"
                     /protein_id="CAA00113.1"
                     /translation="MKFFALTTLLAATASALPTSNPAQELRQLGRTRDLDINGNS
                     ASCADVFIYARGSTETGNTLGPSTASNLESFAGKGVWVGQYRAYRATLGNAL
                     PRGTSSAIREMLGLFOQANTKCPDATLIAGYSQGAALAAASIEDLSAIRDKIAGT
                     VLEGYTKNLQNRGRIPNYPADRTKVFCTNGLVCTGSLIVAAPHLAYGPDARGPAPEF
                     LIKRVAVRGS"
                     269..361
                     /note="cutinase"
                     362..958
                     /product="cutinase"

sig_peptide      269..361
mat_peptide      362..958
ORIGIN            /product="cutinase"

Alignment Scores:
Pred. No.:          2.16e-35      Length:          1121
Score:              546.00      Matches:         108
Percent Similarity: 71.1%      Conservative:    32
Best Local Similarity: 54.8%    Mismatches:     53
Query Match:        54.8%      Indels:          4
DB:                  6          Gaps:           3

US-08-817-997-2_COPY_36_229 (1-194) x A00975 (1-1121)
Qy      1  GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db      356 CAGCTTGGTAGACAACATCGCGAGATCTGATCAACGGCAATAGCGTCTCTCGCGCCGAT 415

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Qy 20 AlaIleuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
Db 416 GTCATCTTCAATTTATGCCGAGGTTCAACAGAGACGGCGCACTTGGGA---ACTCTCGGT 472
Qy 40 ProAlaIleuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrrIleGlnGly 57
Db 473 CTAGACATTCCTCCCAACCTTGAGTCCGCTTCGGCAAGACGGTGTCTGATTCAGGC 532
Qy 58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
Db 533 GTTGGGGTGCCTACCGAGCCACTCTTGGAGACAATGCTCTCCCTCGCGAACCTCTAGC 592
Qy 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
Db 593 GCAGCAATCAGGAGATGCTTGGTCTCTTCAGCAGGCCAACACCAAGTGCCTGACGCG 652
Qy 98 ProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlu 117
Db 653 ACTTTGATCCCGGTGCTACAGCCAGGGTCTGCATTCGACCGCGCTCCATCGAGGAC 712
Qy 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 713 CTCGACTCGGCATTCGTGACAGATCGCGGAAGTCTTCTGTCGGCTACACCAAGAC 772
Qy 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
Db 773 CTACAGAACCGTGGCGAATCCCACTACCTCCGACAGGACCAAGGCTCTTCGCAAT 832
Qy 158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db 833 ACAGGGGATCTCGTTTTGTACTGTAGTCTGATGCTGCTGCACCTCACTTGGCTTATGGT 892
Qy 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 893 CCTGATGCTCGTGGCGCTGCCCTCGAGTTCCTCATCGAAGAGGTTCCGGCT 943
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RESULT 7

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FSOCUT 883 bp mRNA linear PLN 27-APR-1993
LOCUS F. solani pisi (fungus) cutinase mRNA, complete cds.
DEFINITION K02640.1 GI:168145
VERSION cutinase; glycoprotein.
KEYWORDS Fusarium solani
SOURCE Fusarium solani
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 883)
AUTHORS Soliday,C.L., Fluckey,W.H., Okita,T.W. and Kolattukudy,P.E.
TITLE Cloning and structure determination of cDNA for cutinase, an enzyme
involved in fungal penetration of plants
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81, 3939-3943 (1984)
COMMENT Original source text: Fusarium solani pisi (strain T8) cDNA to
mRNA, clones C-[31,4,57].
[1] also sequenced a peptide isolated from a trypsin digest of
cutinase; the amino acid sequence as well as the initiation and
termination codons were used to identify the coding region of the
cDNA.
```

The active serine catalytic triad and a disulfide bridge were located at bases 484 and 688, respectively. Disulfide bridges play an important role in maintaining catalytic activity. The presence of a single disulfide bridge and absence of any SH groups in the mature enzyme shows a discrepancy between this cutinase cDNA sequence and the chemical information concerning the mature enzyme.

FEATURES

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source
    Location/Qualifiers
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            /mol_type="mRNA"
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                79..771
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mRNA
CDS

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VLFGYTKLQNRGRIPNYPADRTKVFCTGTDLVCTGSLIVAAPHLAYGPDARGPAPEF
LIEKRVAVRGSA"
sig_peptide 79..171
mat_peptide 172..768
/product="cutinase"
/115 bp upstream of BglI site.
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ORIGIN

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Alignment Scores:
Pred. No.: 2,036-35 Length: 883
Score: 545.00 Matches: 108
Percent Similarity: 71.1% Conservative: 32
Best Local Similarity: 54.8% Mismatches: 53
Query Match: 54.7% Indels: 4
DB: 15 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x FSOCUT (1-883)

Qy 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db 166 CAGCTTGTGTAGAACAACTCGCGACGATCTGATCAACGGCAATAGCGCTTCTCGCCGAT 225
Qy 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
Db 226 GTCATCTTCAITATGCCCCGAGGTTCAACAGAGACGGGCACTTGGGA---ACTCTCGGT 282
Qy 40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrrIleGlnGly 57
Db 283 CCTAGCATGCTCCAACTTGGTCCGCTTCGGCAAGGCGGTCTCTGGATTACGGGC 342
Qy 58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
Db 343 GTTGGCGGTGCTACCGAGCCACTCTTGGAGACAATGCTCTCCCTCGCGAACCTCTAGC 402
Qy 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
Db 403 GCCCAATACAGGAGATGCTCGGTCTCTTCCAGCAGGCCAACACCAAGTGCCTGACGCG 452
Qy 98 ProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlu 117
Db 463 ACTTTGATCCCGGTGCTACAGCCAGGGTGTCTGCATTCGACCGCGCTCCATCGAGGAC 522
Qy 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 523 CTCGACTCGGCCATTCGTCGACAGATCGCGGAAGTCTTCTGTCGGCTACACCAAGAAC 582
Qy 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
Db 583 CTACAGAACCGTGGCGGAATCCCACTACCTTCGCGCAGCAGGACCAAGGCTCTTCTCAAT 642
Qy 158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db 643 ACAGGGGATCTCGTTTTGTACTGTGAGTCTGATGCTGTCGACCTCAGTGGCTTATGGT 702
Qy 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 703 CCTGATGCTCGTGGCGCTGCCCTCGAGTTCCTCATCGAAGAGGTTCCGGCT 753
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RESULT 8

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COGCUA
LOCUS C.gloeosporioides cutinase gene, complete cds.
DEFINITION M21443
ACCESSION M21443.1 GI:167289
KEYWORDS cutinase.
SOURCE Glomerella cingulata
ORGANISM Glomerella cingulata
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes Incertae sedis; Phyllachorales; Phyllachoraceae;
Glomerella.

1 (bases 1 to 1749)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

Ettinger, W.F., Thukral, S.K. and Kolattukudy, P.E.
Structure of cutinase gene, cDNA, and the derived amino acid
sequence from phytopathogenic fungi
Biochemistry 26, 7883-7892 (1987)
Original source text: C.gloeosporioides DNA (from papaya).
Location/Qualifiers

source

1. 1749
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/db_xref="GI:167290"
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VLEFGYTKNLQNLGRILNPFETSKTEVYCDIADAVCYGTLFILPAHFLYQTDAAVAAPRF
LQARIG"

exon 824..1012
/note="cutinase"
intron 1013..1064
/note="cut intron A"
exon 1065..1550
/note="cutinase"
/number=2

ORIGIN 936 bp upstream of SacI site.

Alignment Scores:

Pred. No.:	4 52e-35	Length:	1749
Score:	544.50	Matches:	110
Percent Similarity:	67.0%	Conservative:	28
Best Local Similarity:	53.4%	Mismatches:	48
Query Match:	54.7%	Indels:	20
DB:	15	Gaps:	2

US-08-817-997-2_COPY_36_229 (1-194) x COGCUYA (1-1749)

QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArg 26
Db 929 AACGAGCTCGAGCCGCGACGAGCTCGCGCTGCCCAAGGTCATCTACATCTTTGCCCGT 988
QY 27 GlySerThrGluProGlyAsnMet----- 34
Db 989 GCCTCGACTGAGCCCGGTAACTGGTAAGGCTTCCTTCATCTTCAAAGCCTATA 1048
QY 35 -----GlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSer-- 48
Db 1049 CTCACATTCGAAAGGAATCAGCAGCAGCCCATCTGTCGCCGAGCCCTGAGAGAAT 1108
QY 49 ----HisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAl 67
Db 1109 CTACGGCGCCAAACAGCTCTGGTTCAGGCGGTGGCGGCCCTTACCTCGCCGACCTGGC 1168
QY 67 aThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPh 87
Db 1169 CTCCAACTTCTGCCCCAGCGCACCTCTGTCGGCGGCCCATCAACGAGCGCCAGCGCTCTT 1228
QY 87 eAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGlnGl 107
Db 1229 CACCTTCGCCAAACACAAAGTGCCCAACGCGGCCCATCTGTCGGCGCGCTACAGCCAGG 1288
QY 107 yAlaAlaLeuIleAlaAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVally 127
Db 1289 CACCGCGGTGATGGCGGCTTCATCTCAGCGCTTGAGCACCACGATCAAGAACCAGATCAA 1348
QY 127 sGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTy 147

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QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
DB 2912 AACGAGCTCGAGACCGGACGAGCTCGCTCGCCCAAGGTCATCTACATCTTTGCCCGT 2971
QY 27 GlySerThrGluProGlyAsnMet----- 34
DB 2972 GCCTCGACTGAGCTGGTAACATGGTAAGGCTTCCTTCGGCCCATCTTCAAGGCCCATTA 3031
QY 35 -----GlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSer-- 48
DB 3032 TTGACATCTCGAATAGGATACGAGCGAGCCCATCTGCGCCAGCCCTTAGAGAAAT 3091
QY 49 ----HisIleArgAsnIleTrpIleGlnGlyValGlyGlyProGlyThrAspAlaLeuAl 67
DB 3092 CTACGGTGCCAAACGAGCTTGGGTCCAGGCGGAGGCGGCTTACCTCGCGGACCTGGC 3151
QY 67 aThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPh 87
DB 3152 CTCCAACTTCTGCGCGACGGCACATCTCTGCGCGCCATCAACGAGGCGGCGCTTTT 3211
QY 87 eAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyThrGlnG 107
DB 3212 CACCTTCGCCAACACAAAGTGCCCAAGCGGCGCATCTCTCGGCGGCTACAGCCAGGG 3271
QY 107 yAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 127
DB 3272 CACCGCGGTGATCGCGGCTCCATCTCCGGCCTGAGCACCCAGCATCAAGAACCCAGATCAA 3331
QY 127 sGlyValAlaLeuPheGlyThrGlnAnLeuGlnAnArgGlyGlyIleAlaGln 147
DB 3332 GGGCGTGTGCTCTTCGGGTACACCAAGAACCTGCAGAACCTGGCGCGCATCCCAACTT 3391
QY 147 rProArgGluArgThrLysValPheCysAnValGlyAspAlaValCysThrGlyThrLe 167
DB 3392 CGAGAGCTCCAGACCGAGGTCTACTGGGACATTCGGGCGCGTCTGCTACGGCACCT 3451
QY 167 uIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArgPh 187
DB 3452 GTTCATCTCTCGCGCGACCTTTTGTACAGACTGATGCGGCTGTTCGGCGCCCGCGATT 3511
QY 187 eLeuArgAspArgIle 192
DB 3512 CTTCCAGGCGCGCATT 3527

RESULT 10
FSU63335
LOCUS Nectria ipomoeae cutinase (cutA) gene, complete cds.
DEFINITION Nectria ipomoeae 3938 bp DNA linear PLN 14-JUN-2002
ACCESSION U63335
VERSION U63335.1 GI:1488294
KEYWORDS
SOURCE Nectria ipomoeae
ORGANISM Nectria ipomoeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 3938)
AUTHORS Crowhurst,R.N., Binnie,S.J., Bowen,J.K., Hawthorne,B.T.,
Plummer,K.M., Rees-George,J., Rikkerink,E.H. and Templeton,M.D.
EFFECT of disruption of a cutinase gene (cutA) on virulence and
tissue specificity of Fusarium solani f. sp. cucurbitae race 2
toward Cucurbita maxima and C. moschata
Mol. Plant Microbe Interact. 10 (3), 355-368 (1997)
JOURNAL 9100380
PUBMED 2 (bases 1 to 3938)
REFERENCE Crowhurst,R.N.
AUTHORS Direct Submission
TITLE Submitted (09-JUL-1996) Plant Improvement Division, HortResearch,
JOURNAL 120 Mt Albert Rd., Auckland, New Zealand
FEATURES
source Location/Qualifiers
1..3938
/organism="Nectria ipomoeae"
/mol_type="genomic DNA"
/strain="PGB 153"
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/ncbi="taxon:57162"
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/product="cutinase"
/protein_id="AAB05922.1"
/db_xref="GI:1488295"
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PRGYSRAIRMLGLFOQANTKCPDATALAGYSQGAALAAASIELDLSAIRDKIAGT
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Alignment Scores:
Pred. No.: 1.19e-33 Length: 3938
Score: 531.50 Matches: 109
Percent Similarity: 65.9% Conservative: 32
Best Local Similarity: 50.9% Mismatches: 52
Query Match: 53.4% Indels: 21
DB: 15 Gaps: 4

US-08-817-997-2_COPY_36_229 (1-194) x FSU63335 (1-3938)
QY 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
DB 2216 CAGCTTGGTAGAACAACTCGGACGATCTGATCAACGGCAACAGCGCTTCTCGCGCGAT 2275
QY 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMet----- 34
DB 2276 GTCATCTTCAATTATGCGCGAGGTTCAACAGAGACGGGCAACTTGGTTTCGTAGATTGT 2335
QY 35 -----GlyIleThrValGlyProAlaLeu 42
DB 2336 TCTGATTACAACACCACCTTCTTACATACATACATTAGGGA---ACACTCGGTCGAGCATC 2392
QY 43 AlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyValGly 60
DB 2393 GCCTCCAACTTGTAGTCCGCTTCGGAAAGGACGGTGTGATCCAGGCGGTTCGGCT 2452
QY 61 ProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle 80
DB 2453 GCCTACCGAGCCACTCTTGGGACAAACGCTCTGCCCGCGGAACCTCTAGCGCGCATC 2512
QY 81 AspGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValVal 100
DB 2513 CGGGAGATGCTCGGTCTCTCCAGCAGGCCAACACCAAGTGCCTGACGCGACTCTGATC 2572
QY 101 AlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGly 120
DB 2573 GCCGGTGTCTACAGCGGCTGCTGATTCGAGCGGCTTCATCGAGGACCTTGATCG 2632
QY 121 AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn 140
DB 2633 GCTATTGCGACAGATCGCGGACTCTTCTGTTGGCTACCAAGAACCTGCGAGAAC 2692
QY 141 ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp 160
DB 2693 CGTGGCGGAATTCCCACTACCTGCTGCAGGACCAAGGCTCTCTGCAACGCTGGCGAT 2752
QY 161 AlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAla 180
DB 2753 CTCGTTTGCACCGGTAGCTTGTCTGCTGCACCTTCATCTGGCTATGCTCTGATGCT 2812
QY 181 ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
DB 2813 CGTGCGCTCTGCCCTGAGTTCTTATCGAAGAGGTTCGGCT 2854

RESULT 11
COGCTUB
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LOCUS COGUTB 2557 bp DNA linear PLN 27-APR-1993
DEFINITION C.capsici cutinase gene, complete cds.
ACCESSION M18033
VERSION M18033.1 GI:167291
KEYWORDS cutinase.
SOURCE Colletotrichum capsici
ORGANISM Colletotrichum capsici
REFERENCE 1 (bases 1 to 2557)
AUTHORS Ettinger, W.F., Thukral, S.K. and Kolattukudy, P.E.
TITLE Structure of cutinase gene, cDNA, and the derived amino acid sequence from phytopathogenic fungi
JOURNAL Biochemistry 26, 7883-7892 (1987)
COMMENT Original source text: C.capsici DNA (from papaya).
FEATURES Location/Qualifiers
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 1054..>1542
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ORIGIN 5 bp upstream of PstI site.

Alignment Scores:
 Pred. No.: 8.4e-34 Length: 2557
 Score: 531.00 Matches: 108
 Percent Similarity: 64.9% Conservative: 27
 Best Local Similarity: 51.9% Mismatches: 51
 Query Match: 53.3% Indels: 22
 DB: 15 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x COGUTB (1-2557)

 Qy 7 AaNGlyLeuGluSerGlySerAlaAaenAlaCysProAspAlaIleLeuIlePheAlaArg 26
 Db 913 AAGAGCTTGAAGTCGGCAGCAGCTCCAACTGCCCAAGGTCATCATCTTTGCTCGC 972

 Qy 27 GlySerThrGluProGlyAenMet----- 34
 Db 973 GCCTTACTGAGCCCGGTACATGTTAAGTCAGTCAGTCAGCGTCTCCCTTCCACAGGAT 1032

 Qy 35 -----GlyIleThrValGlyProAlaLeuAlaAaenGlyLeuGlu 47
 Db 1033 GATAACTGACTCTATACAGGCGCATCAGCGCAGGCCCATTTGTCGCGAGCTCTCGAA 1092

 Qy 48 SerHis-----IleArgAenIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAa 65
 Db 1093 AGCCGCTACGCGCCCTCACAGGTCCTGGGTCAGGCGGTTGGCGGCCCTTACTCTCGCGAC 1152

 Qy 66 LeuAlaThrAaenPhe---LeuProArgGlyThrSerGlnAlaAaenIleAaenGlyGlyLys 84
 Db 1153 CTGGCTTCAACTTCATCATACCGGAGGCGACCTCCCGCGCTGCCATCAACGAGGCTTAAG 1212

 Qy 85 ArgLeuPheAlaLeuAlaAaenGlnLysCysProAsnThrProValValAlaIleGlyTyr 104

Db 1213 CGACTCTTACGCTCGCAACACCAACTGCGCCGCTGCTCGCAGGCGGATAC 1272
Qy 105 SerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGlu 124
 |||||
Db 1273 AGCAGGGCACAGCGGTGATGCGCTCTCCATCTCCGAGTTGAGCTCCACGATCCAGAAC 1332

Qy 125 GlnValLysGlyValAlaLeuPheGlyTyrThrGlnAenLeuGlnAaenArgGlyGlyIle 144
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Db 1333 CAGATCAAGGGCGTCTGTCGGCTATATACCAAGAACCTTCGACAACTTGGAGCGCATC 1392

Qy 145 AlaAsnTyrProArgGluArgThrLysValPheCysAenValGlyAspAlaValCysThr 164
 |||||
Db 1393 CCGACTTCTCGACATCCAGACCGAGGTGTACTGTGCGCTCGCGATGCTGTGCTATC 1452

Qy 165 GlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaAaenGlyGluAla 184
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Db 1453 GGCACGCTGTTTCATCTCGCGCGCATTTCTTGTATCAACAGCGCATGCTCTCTGCC 1512

Qy 185 AlaArgPheLeuArgAspArgIle 192
Db 1513 CCGAGATTCTCTTGTCTCTCGCAT 1536

RESULT 12
AF417004
LOCUS AF417004 1735 bp DNA linear PLN 14-JUN-2002
DEFINITION Nectria haematococca cutinase 2 (cut2) gene, complete cds.
ACCESSION AF417004
VERSION AF417004.1 GI:16417361
KEYWORDS
SOURCE Nectria haematococca (anamorph: Fusarium solani f. sp. pisi)
ORGANISM Nectria haematococca
REFERENCE 1 (bases 1 to 1735)
AUTHORS Li, D., Sirakova, T., Rogers, L., Ettinger, W.F. and Kolattukudy, P.E.
TITLE Regulation of constitutively expressed and induced cutinase genes by different zinc finger transcription factors in Fusarium solani f. sp. pisi (Nectria haematococca)
JOURNAL J. Biol. Chem. 277 (10), 7905-7912 (2002)
REFERENCE 1175644
AUTHORS 2 (bases 1 to 1735)
TITLE Sirakova, T. and Kolattukudy, P.E.
JOURNAL Direct Submission
 Submitted (05-SEP-2001) Neurobiotechnology Center, The Ohio State University, 206 Rightmire Hall, 1060 Carmack Road, Columbus, OH 43210, USA
FEATURES Location/Qualifiers
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 /note="anamorph: Fusarium solani f. sp. pisi"
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 /product="cutinase 2"
 join(405..599,649..1149)
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 /note="esterase; active serine type"
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 FLIEKVPVRGSA"
ORIGIN
Alignment Scores:

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Pred. No.: 4.86e-33 Length: 1735
Score: 519.50 Matches: 106
Percent Similarity: 65.2% Conservatives: 31
Best Local Similarity: 50.5% Mismatches: 55
Query Match: 52.2% Indels: 18
DB: 15 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x AF417004 (1-1735)

Qy 3 GlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeu 22
Db 504 GGAACACCCGCAACGATCTTACCAACGCAACAGCGCTTCTTGGCGCGATGTAATCTTT 563
Qy 23 IlePheAlaArgGlySerThrGluProGlyAsnMet-GlyIle----- 36
Db 564 ATCTATGCCGCGAGGTTCAACTGAGACGGCACTTGTCGCTAGACTCTGTTCCAATGGC 623
Qy 37 -----ThrValGlyProAlaLeuAlaAsnGlyLeuG1 47
Db 624 AACATCACTCTCACATACACTAGGAACTCTTGGCCCCCAGCATCGCCTCCAAGCTCGA 683
Qy 47 uSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaA1 65
Db 684 GTCCGCTTCGGCAGGACGGCTCTGGATTCAAGGGGTTGGCGTCCCTACCGAGCCAC 743
Qy 65 aLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysAr 85
Db 744 TCTTGGAGACAATTCCTCCCGCGGCACTCTAGCGCGCCCATCAGGGAGATGCTCGG 803
Qy 85 gLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSe 105
Db 804 TCTCTTCCAGCAGGCAACACCAAGTCCCGGACGCACTCTGATCGCGGTGGCTACAG 863
Qy 105 rGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluG1 125
Db 864 CCAGGTGGCGACTTGGAGTCCCTCCGCGAGGACCTCGACTCGGCCATTCGTCGACAA 923
Qy 125 nValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleA1 145
Db 924 GATCGCGGGGACGGTCTGTTGCGTACTACTAGAACCTGCAGACACCGCGCATCCC 983
Qy 145 aAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrG1 165
Db 984 AAACCTTCCCTGCTGATAGAACCAAGGCTTCTGCAACACTGTGTGATCTGTATGCA 1043
Qy 165 yThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaA1 185
Db 1044 TTCCTTGATCATGTGCGCGCTCACCTTACTTATGTCTGACGCTGTCGCGCGAGCCC 1103
Qy 185 aArgPheLeuArgAspArgIleArgAla 194
Db 1104 TGAGTTCCTTATAGAAAGTTGAGCT 1131

RESULT 13
LOCUS FSOCUTA
DEFINITION F. solani cutinase gene, complete cds.
ACCESSION M29759
VERSION M29759.1 GI:168147
KEYWORDS cutinase.
SOURCE Fusarium solani
ORGANISM Fusarium solani
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
REFERENCE 1 (bases 1 to 2769)
AUTHORS Soliday, C.L., Dickman, M.B. and Kolattukudy, P.E.
TITLE Structure of the cutinase gene and detection of promoter activity
in the 5'-flanking region by fungal transformation
JOURNAL J. Bacteriol. 171 (4), 1942-1951 (1989)
PUBMED 2703464
COMMENT Original source text: F. solani (f. sp. pisi (Nectria hematococa)
DNA.
FEATURES
Location/Qualifiers
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Db	1591	CGTTTGACTGCGTAGCTTGATGACCTTGCTGCACCTCACTTGGCTATTGGTCTGCTGCTGCTG 1650
Qy	181	gGlyGluAlaAalaAargPheLeuAargAspArgIleArgAla 194
Db	1651	TGGCCCTGCGCCTGAGTTCCTCATCGAGAAGTTCGGCT 1690
RESULT 14		
ARCUT		
LOCUS	A.rabiei	cut gene for cutinase.
DEFINITION	X65628	1662 bp DNA linear
ACCESSION	X65628.1	PLN 18-APR-2005
VERSION		
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
AUTHORS	1 (bases 1 to 1662)	
TITLE	Margolles-Clark,E., Tenkanen,M., Soderlund,H. and Penttila,M. Acetyl xylan esterase from Trichoderma reesei contains an active-site serine residue and a cellulose-binding domain	
JOURNAL	Eur. J. Biochem. 237 (3), 553-560 (1996)	
PUBMED	8647098	
REFERENCE	2 (bases 1 to 1662)	
AUTHORS	Tenhaken,R. and Barz,W.	
TITLE	Characterization and cloning of cutinase from ascochyta rabiei	
JOURNAL	Unpublished	
REFERENCE	3 (bases 1 to 1662)	
AUTHORS	Tenhaken,R.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-APR-1992) R. Tenhaken, Institut fuer Biochemie und Biotechnologie der Pflanzen, Hindenburgplatz 55, D-4400 Muenster, FRG	
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ORIGIN		
Alignment Scores:	5.61e-33	1662
Pred. No.:	518.50	112
Score:		

University, 206 Rightmire Hall, 1060 Carmack Road, Columbus, OH
43210, USA

FEATURES

source Location/Qualifiers
1..1697
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/note="esterase; active serine type"
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/product="cutinase 3"
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FLIEKVRVRGSA"

ORIGIN

Alignment Scores:
Pred. No.: 6,91e-33 Length: 1697
Score: 517.50 Matches: 105
Percent Similarity: 64.8% Conservative: 31
Best Local Similarity: 50.0% Mismatches: 56
Query Match: 52.0% Indels: 18
DB: 15 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x AF417005 (1-1697)

QY 3 GlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeu 22
Db 504 GGAACACCCGCAACGATCTTACCAACGCGACGCGCTTCTGCGCCGATGTAATCTTT 563
QY 23 IlePheAlaArgGlySerThrGluProGlyAsnMet-GlyIle----- 36
Db 564 ATCTATGCCGAGGTTCAACTGAGACGGGCAACTTGTGTCGTAGACTCTGTTTCCAATGGC 623
QY 37 -----ThrValGlyProAlaLeuAlaAsnGlyLeuGl 47
Db 624 AACATCACTCTCACATACACTAGGGAACCTCTTGGCCCCAGCATCGCTCCAAGCTCGA 683
QY 47 uSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaI 65
Db 684 GTCCGCTTCGGCAGGCGGCTCTGGATTAGGCGGTGGCGGTGCTTACCGAGCCAC 743
QY 65 aLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysAr 85
Db 744 TCTTGAGACAATTCCTCCCGCGGAACCTCTAGCGCGGCATCAGGAGATGCTCGG 803
QY 85 gLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyClyTyrSe 105
Db 804 TCTCTTCCAGCAGCCAAACCAAGTGCCTCCGAGGACCTCGACTCGCGGTGGCTACAG 863
QY 105 rGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGl 125
Db 864 CAGGTCGCGGCACCTTGCAGTGCCTCCGTCGAGGACCTCGACTCGGCCATCCGTGACAA 923
QY 125 nValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyClyIleAl 145
Db 924 GATCGCGGACCGTCTCTGTTGGCTAGACTAGAACTTGCAACACCGCGCGAATCCC 983
QY 145 aAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGl 165
Db 984 AAACCTCCCTGCTGATAGAACCAAGGCTCTTCTGCAACACTGGTGTATCTCGTATGCACAG 1043

QY 165 yThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAl 185
Db 1044 TTCTTGATCATTCGCTGCGCTCACCTTACTTATGCTCTGACGCTCGTGGCCCGCC 1103
QY 185 aArgPheLeuArgAspArgIleArgAla 194
Db 1104 TGAGTTCTTATTGAGAAGGTTCGAGCT 1131

Search completed: February 4, 2006, 23:14:33
Job time : 4853 secs

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2006, 20:47:09 ; Search time 587 Seconds
(without alignments)
2202.641 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QGATENGLESANACPD.....SYTIARGEARFLDRIRA 194

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-USER=us08817997 @CGN 1.1 727 @runat_03022006_161325_17986 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
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12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	996	100.0	1016	2 AAT29401	Aat29401 Lipase co
2	546	54.8	718	2 AAQ68591	Aaq68591 Synthetic
3	546	54.8	718	2 AAQ57027	Aaq57027 Synthetic
4	546	54.8	718	2 AAQ68583	Aaq68583 Synthetic

5	546	54.8	1121	2 AAQ05859	Aaq05859 Cutinase
6	519.5	52.2	2769	12 ADH34524	Adh34524 Fusarium
7	506	50.8	789	12 ADL27534	Adl27534 cDNA sequ
8	500.5	50.3	914	2 AAT95844	Aat95844 Gliocladi
9	499.5	50.2	999	2 AAT95846	Aat95846 Trichopha
10	497.5	49.9	675	12 ADN89479	Adn89479 A. oryzae
11	482	48.4	869	2 AAT95845	Aat95845 Verticill
12	455.5	45.7	780	12 ADN89480	Adn89480 A. oryzae
13	430	43.2	2371	12 ADL27533	Adl27533 Genomic s
14	262	26.3	280	2 AAQ68590	Aaq68590 Cassette
15	262	26.3	280	2 AAQ68582	Aaq68582 Cassette
16	260	26.1	768	12 ADH47688	Adh47688 DNA encod
17	260	26.1	798	4 AAF23513	Aaf23513 DNA encod
18	260	26.1	798	6 ABK53022	Abk53022 Aspergill
19	260	26.1	798	12 ADK70254	Adk70254 Aspergill
20	240	24.1	275	2 AAQ57026	Aaq57026 pur7208,
21	212	21.3	242	2 AAQ57025	Aaq57025 pur7208,
22	212	21.3	246	2 AAQ68589	Aaq68589 Cassette
23	212	21.3	246	2 AAQ68581	Aaq68581 Cassette
24	192	19.3	1025	8 ABX13438	Abx13438 A. oryzae
25	189.5	19.0	651	13 ADR96587	Adr96587 M. tuberc
26	189.5	19.0	654	2 AAX34071	Aax34071 Mycobacte
27	189.5	19.0	654	13 ADU16604	Adu16604 M. tuberc
28	189.5	19.0	654	14 AEB92000	Aeb92000 DNA encod
29	189.5	19.0	720	2 AAX34072	Aax34072 Mycobacte
30	189.5	19.0	720	13 ADU16606	Adu16606 M. tuberc
31	189.5	19.0	1054	2 AAV63919	Aav63919 Mycobacte
32	189.5	19.0	1054	2 AAX81005	Aax81005 Nucleotid
33	189.5	19.0	15239	2 AAT33536	Aat33536 BCG delet
34	189.5	19.0	110000	4 AAI99682_22	Continuation (23 o
35	189.5	19.0	110000	4 AAI99683_22	Continuation (23 o
36	188.5	18.9	1060	2 AAV63921	Aav63921 Mycobacte
37	188.5	18.9	1060	2 AAX81007	Aax81007 Nucleotid
38	188.5	18.9	110000	4 AAI99682_25	Continuation (26 o
39	188.5	18.9	110000	4 AAI99683_25	Continuation (26 o
40	178	17.9	800	2 AAX81033	Aax81033 Nucleotid
41	178	17.9	800	2 AAX81033	Aax81033 Nucleotid
42	178	17.9	110000	4 AAI99682_38	Continuation (39 o
43	178	17.9	110000	4 AAI99683_38	Continuation (39 o
44	168	16.9	110000	4 AAI99682_41	Continuation (42 o
45	168	16.9	110000	4 AAI99683_41	Continuation (42 o

ALIGNMENTS

RESULT 1
AAT29401
ID AAT29401 standard; DNA; 1016 BP.

AC AAT29401;

DT 17-DEC-1996 (first entry)

XX Lipase coding sequence.

DE Lipase; detergent; dishwashing; laundry; short-chain lipid; ss.

XX Humicola insolens.

XX Key Location/Qualifiers
FH CDS 43..783
FT /*tag= a
FT /*note= "immature protein"
FT sig_peptide 43..147
FT mat_peptide 148..780
FT /*tag= b
FT /*tag= c

PN WO9613580-A1.

XX 09-MAY-1996.

PF 26-OCT-1995; 95WO-DK000427.

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XX 26-OCT-1994; 94DK-00001240.
XX (NOVO ) NOVO-NORDISK AS.
XX Sandal T, Kauppinen S, Kofod LV;
XX WPI; 1996-239493/24.
XX P-PSDB; AAR95051.
XX Isolated DNA encoding lipolytic enzyme - derived from Humicola insolens
XX DSM1800, used partic. as detergent additive for laundry and dishwashing
XX compens.
XX Claim 1; Page 51; 63pp; English.
XX The present sequence encodes an enzyme with lipolytic activity, derived
XX from Humicola insolens DSM1800. The enzyme has a mol. wt. of about 20-21
XX kDa, a pI in the range of 709, a pH optimum of about 8 and has
XX specificity towards short-chain lipid substrates. It can be used as a
XX detergent additive, partic. in compens. for laundry washing or
XX dishwashing
XX SQ Sequence 1016 BP; 231 A; 319 C; 289 G; 177 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.11e-99 Length: 1016
Score: 996.00 Matches: 194
Percent Similarity: 100.0% Conservativity: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x AAT29401 (1-1016)

Qy 1 GlnLeuGlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAla 20
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Qy 21 IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyPro 40
Db 208 ATCTGATCTTTGCTGCGGCTCGACCGAGCGAGGCAACATGGGCATCACCGTCGGCCCT 267
Qy 41 AlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGly 60
Db 268 GCTCTGCCACAGCGCTTGAATCCCATCCGACATCCGACATCTGGATCCAGGCGGTGGCGGC 327
Qy 61 ProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle 80
Db 328 CCTTACGACCGCGCTGGCCACCACTTCTGCGGCGGCACCTCGCAGGCGCAACATC 387
Qy 81 AspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValVal 100
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Qy 101 AlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGly 120
Db 448 GCCGGGGGTACAGCCAGGCGCGGCGCTCATGCTGCCCGCGCTCAGCGAGCTCAGCGGC 507
Qy 121 AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn 140
Db 508 GCCGTCAAGGAGCAGGTCAAGGGCGTCCCTCTTCGATACACCCAAACCTCCAGAAC 567
Qy 141 ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp 160
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Qy 161 AlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAla 180
Db 628 GCCGTTCGACCGGACGCTCATCATCCCGCGGCATCTGTGTCACGATCGAGGCG 687
Qy 181 ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194

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Db 688 CGCGGTGAGCGCGAGGTTCTCTGCGGATCGCATCCGTGCT 729

RESULT 2
AAQ68591
ID AAQ68591 standard; DNA; 718 BP.
XX AC AAQ68591;
XX 25-MAR-2003 (revised)
DT 03-MAR-1995 (first entry)
XX Synthetic gene encoding Fusarium solani pisi pre-pro-cutinase.
XX Synthetic gene; cutinase; cassette; ds.
XX Synthetic.
XX Key Location/Qualifiers
CDS 16..63
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/product= "pre-sequence"
CDS 64..108
/*tag= b
/product= "pro-sequence"
FT mat_peptide 109..708
/*tag= c
WO9414964-A1.
XX 07-JUL-1994.
XX 09-DEC-1993; 93WO-EP003551.
XX 23-DEC-1992; 92EP-00204079.
XX (UNIL ) UNILEVER NV.
XX (UNIL ) UNILEVER PLC.
XX Egmond MR, Van Der Hijden HTWM, Musters W, Peters H, Verrips CT;
XX De Vlieg J;
XX WPI; 1994-234699/28.
XX P-PSDB; AAR59801.
XX Eukaryotic cutinase variants with improved lipolytic activity - with
XX modified amino acid structure to improve compatibility with anionic
XX surfactants.
XX Example; Fig 1D; 72pp; English.
XX A synthetic gene encoding Fusarium solani pisi pre-pro-cutinase was
XX produced by assembly of three separate cassettes starting from synthetic
XX DNA oligos. The synthetic cutinase gene was assembled and yielded PUR7210
XX which comprises an ORF encoding the complete pre-pro-cutinase of F.
XX solani pisi. (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 718 BP; 144 A; 223 C; 190 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.2e-50 Length: 718
Score: 546.00 Matches: 108
Percent Similarity: 71.1% Conservativity: 32
Best Local Similarity: 54.8% Mismatches: 53
Query Match: 54.8% Indels: 4
DB: 2 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x AAQ68591 (1-718)

Qy 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db 103 CAGCTTGTGTATACAACTCGCGCAGATCTGATCAACGGCAATAGCGCTTCCTGCGCCGAT 162
Qy 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39

```

```

Db 163 GTCACTTTCATTTATGCTCGAGGTTCAACAGAGACGGGCACTTGGGA---ACTCTCGGG 219
Qy 40 ProAlaLeuAlaAenGlyLeuGluSerHisIle-----ArgAenIleTrpIleGlnGly 57
Db 220 CCCAGCATGCTCCCAACCTTGAGTCGCCCTTCGGCAAGACGGTGCTCGATTCAGGGC 279
Qy 58 ValGlyGlyProTyrAspAlaLeuAlaThrAsnPhelLeuProArgGlyThrSerGln 77
Db 280 GTTGGCGGTGCTCCACGAGCCACCTTAGGAGACATGCTCTCCGCGGGGAACCTCTAGC 339
Qy 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAenGlnLysCysProAsnThr 97
Db 340 GCCGCATCAGGAGATGCTAGGCTCTTCACAGAGCCCAACCAAGTGCCTGACGCG 399
Qy 98 ProValValAlaGlyTyrSerGlnGlyAlaLeuAlaLeuIleAlaAlaValSerGlu 117
Db 400 ACTTTGATCGCGGTGGCTACAGCCAGGGTGCTGCACCTTCAGCGCGCTAGCATCGAGGAC 459
Qy 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 460 CTCGACTCGGCCATTCGTGACAAAGATCGCGGTACCGTTCTGTTCGGCTACACCAAGAAC 519
Qy 138 LeuGlnAsnArgGlyGlyIleAlaAenTyrProArgGluArgThrLysValPheCysAsn 157
Db 520 CTACAGAAATCGCGCGGCAATCCCACTACCTCGCAGACAGGACCAAGGTCTTCGCAAT 579
Qy 158 ValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThr 177
Db 580 ACAGGAGATCTCGTTTGACTGTAGTGTGATGCTGCTGCACCTCACTTGGCATATGGT 639
Qy 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 640 CCTGATGCCCGGGGACTGCGCCCTGAGTTCTCATCGAGAGAGTTCGGGCT 690

RESULT 3
AAQ57027
ID AAQ57027 standard; DNA; 718 BP.
XX AC AAQ57027;
XX AT 25-MAR-2003 (revised)
XX DT 10-AUG-1994 (first entry)
XX DE Synthetic F. solani pisi cutinase gene.
XX KW Cassette 1; cassette 2; cassette 3; Fusarium solani pisi; cutinase; gene;
XX KW enzyme; enzymatic; detergent; composition; surfactant; anionic; nonionic;
XX KW lipolytic activity; wash cycle; wash process; automatic; washing machine;
XX KW tumble drier; ds.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX CDS 16..708
XX FT /*tag a
XX FT /product= "Pre-pro-cutinase"
XX FT sig_peptide 16..62
XX FT /*tag b
XX FT /note= "Pre-sequence"
XX FT misc_feature 63..107
XX FT /*tag c
XX FT /note= "Pro-sequence"
XX FT mat_peptide 108..708
XX FT /*tag d
XX FT /note= "Mature cutinase"
XX PN W09403578-A1.
XX XX
XX PD 17-FEB-1994.
XX XX
XX PF 20-JUL-1993; 93WO-BF001923.
XX XX

```

```

PR 31-JUL-1992; 92GB-00016387.
XX (UNIL ) UNILEVER PLC.
PA (UNIL ) UNILEVER NV.
XX Van Der Hijden HTWM, Marugg JD, Warr JF, Klugkist J, Musters W;
PI Hondmann DHA;
XX WPI; 1994-065669/08.
DR P-PSDB; AAR46295.
XX Enzyme-contg. detergent compns. - comprises anionic-nonionic surfactant
XX system, and a lipolytic enzyme pref. a fungal cutinase derived from F.
XX solani pisi.
XX Disclosure; Fig 1D; 67pp; English.
XX This sequence represents the full length synthetic Fusarium solani pisi
XX cutinase gene which was constructed using the sequences given in AAQ57024
XX -26 which represent cutinase cassettes 1-3. The full length cutinase gene
XX was used in the production of the cutinase enzyme for use in an enzymatic
XX detergent composition. The composition also comprises (by wt.) 0.1-50% of
XX a surfactant system comprising 0-95% of 1 or more anionic surfactants and
XX 5-100% of 1 or more nonionic surfactants. The composition exhibits a
XX substantial lipolytic activity during the main cycle of a wash process in
XX an automatic washing machine, and consequently produces lipolytic
XX activity when used to wash fabrics which have not been in contact with
XX the detergent product before. The composition is also especially suitable
XX for use in combination with a tumble drier. (Updated on 25-MAR-2003 to
XX correct FN field.)
XX SQ Sequence 718 BP; 144 A; 223 C; 191 G; 160 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,2e-50 Length: 718
Score: 546.00 Matches: 108
Percent Similarity: 71.1% Conservative: 32
Best Local Similarity: 54.8% Mismatches: 53
Query Match: 54.8% Indels: 4
DB: 2 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x AAQ57027 (1-718)
Qy 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db 103 CAGCTTGGTAGACAACACTCGCGACGATCTGATCAACGCAATAGCGTCTCTCGCGCGAT 162
Qy 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
Db 163 GTCACTTTCATTTATGCTCGAGGTTCAACAGAGACGGGCACTTGGGA---ACTCTCGGG 219
Qy 40 ProAlaLeuAlaAenGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
Db 220 CCCAGCATGCTCCCAACCTTGAGTCCGCCCTTCGGCAAGACGGTGCTCGATTCAGGGC 279
Qy 58 ValGlyGlyProTyrAspAlaLeuAlaLeuAlaThrAsnPhelLeuProArgGlyThrSerGln 77
Db 280 GTTGGCGGTGCTTACCGAGCCACCTTAGGAGACATGCTCTCCGCGGGGAACCTCTAGC 339
Qy 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAenGlnLysCysProAsnThr 97
Db 340 GCCGCATCAGGAGATGCTAGGCTCTTCACAGAGCCCAACCAAGTGCCTGACGCG 399
Qy 98 ProValValAlaGlyTyrSerGlnGlyAlaLeuAlaLeuIleAlaAlaValSerGlu 117
Db 400 ACTTTGATCGCGGTGGCTACAGCGAGGTGCTGCACTTGGACCGCTAGCATCGAGGAC 459
Qy 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 460 CTCGACTCGGCCATTCGTGACAAAGATCGCGGTACCGTTCTGTTCGGCTACACCAAGAAC 519
Qy 138 LeuGlnAsnArgGlyGlyIleAlaAenTyrProArgGluArgThrLysValPheCysAsn 157

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Db 520 CTACAGATCGCGCGGAATCCCACTACCTCCGCGCAGGACCAAGTCTTCTGCAAT 579
QY 158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db 580 ACAGAGAGTCTGTTGTACTGTGTAGTCTGTGCTGCTGCACCTCACTTGGCATATGGT 639
QY 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 640 CCTGATGCCCGGGGACCTGCCCTGAGTTCTCTCATCGAGAAGGTTCCGGGT 690

RESULT 4
AAQ05853
ID AAQ05853 standard; DNA; 718 BP.
XX
AC AAQ05853;
DT 25-MAR-2003 (revised)
DT 02-MAR-1995 (first entry)
XX
XX Synthetic gene encoding Fusarium solani pisi pre-pro cutinase.
XX
XX Synthetic gene; cutinase; cassette; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 16..63
XX /tag= a
XX /product= "pre-sequence"
XX CDS 64..108
XX /tag= b
XX /product= "pro-sequence"
XX mat_peptide 109..708
XX /tag= c
XX
XX WO9414963-A1.
XX
XX 07-JUL-1994.
XX
XX 09-DEC-1993; 93WO-BP003550.
XX
XX 18-DEC-1992; 92EP-00204025.
XX
XX (UNIL ) UNILEVER PLC.
XX (UNIL ) UNILEVER NV.
XX
XX Egmond MR, Van Der Hijden HTWM, Musters W, Peters H, Verrips CT;
XX De Vlieg J;
XX
XX WPI: 1994-234698/28.
XX P-PSDB; AAR59796.
XX
XX Eukaryotic cutinase variants with improved lipolytic activity - useful in
XX detergent compans., with modified amino acid compsn. to increase
XX hydrophobicity.
XX
XX Example; Fig 1D; 77pp; English.
XX
XX A synthetic gene encoding Fusarium solani pisi pre-pro-cutinase was
XX performed by assembly of three separate cassettes starting from synthetic
XX DNA oligos. The synthetic cutinase gene was assembled and yielded pUR7210
XX which comprises an ORF encoding the complete pre-pro-cutinase of F.
XX solani pisi. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 718 BP; 144 A; 223 C; 190 G; 161 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,2e-50 Length: 718
Score: 546.00 Matches: 108
Percent Similarity: 71.1% Conservative: 32
Best Local Similarity: 54.8% Mismatches: 53
Query Match: 54.8% Indels: 4
DB: 2 Gaps: 3

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US-08-817-997-2_copy_36_229 (1-194) x AAQ05853 (1-718)
QY 1 GlnLeuGly---AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
Db 103 CAGCTTGGTATACAACTCGCGACGATCTGATCAACGCGCAATAGCGCTTCTCGCCGAT 162
QY 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
Db 163 GTCATCTTCAATTTATGCTCGAGGTTCAACAGAGACGGGCAACTTGGGA---ACTCTCGG 219
QY 40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGly 57
Db 220 CCAGCATTCGCTCCAACTTGAAGTCCGCTTCGCGCAAGGACGGTGTCTGGATTGAGGC 279
QY 58 ValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
Db 280 GTTGGCGGTGCTTACCGAGCCACCCTAGGAGACAATGCTCTCCGCGGGGAACCTCTAGC 339
QY 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
Db 340 GCCGCAATCAGGAGATGCTAGGCTCTTCCAGCAGGCGCAACACCAAGTCCCTCAGCG 399
QY 98 ProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGlu 117
Db 400 ACTTTGATCGCGGTGCTACAGCAGGCTGCTGCACCTTGCAGCGCTAGCATCCAGGAC 459
QY 118 LeuSerGlyAlaValLysGluInValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
Db 460 CTGACTCGGCCATTCGTGACAGATCGCGGTACCGTCTCTGTCGGGTACACCAAGAAC 519
QY 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
Db 520 CTACAGAAATCGCGCGCAATCCCACTACCTCCGACGAGACCAAGGTCTTCTGCAAT 579
QY 158 ValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db 580 ACAGGAGATCTCGTTTGTACTGTGAGTGTGATCGTTCGTGCACCTCACTTGGCATATGGT 639
QY 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 640 CTTGATGCCCGGGGACCTGCCCTGAGTTCTCTCATCGAGAAGGTTCCGGGT 690

RESULT 5
AAQ05859
ID AAQ05859 standard; cDNA; 1121 BP.
XX
AC AAQ05859;
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-JAN-1991 (first entry)
XX
XX Cutinase gene of Fusarium solani pisi.
XX cutinase; bridging peptide; acidolysis; alcohololysis; ss.
XX Fusarium solani; pisi.
XX
XX Key Location/Qualifiers
XX CDS 269..962
XX /tag= a
XX /product= "cutinase"
XX /note= "putative"
XX sig_peptide 269..317
XX /tag= b
XX misc_feature 317..361
XX /tag= c
XX /label= bridging sequence
XX
XX WO9009446-A.
XX
XX 23-AUG-1990.

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XX 17-FEB-1989; 89EP-00400462.
 XX 17-FEB-1989; 89EP-00400462.
 PR (PLAN-) PLANT GENETICS SYST.
 XX Degeus P;
 XX WPI; 1990-275135/36.
 DR P-PSDB; AAR06610.
 XX Pure recombinant cutinase and derivs. - used for hydrolysing or
 PT synthesising ester(s) or for alcoholysis or acidolysis.
 XX Disclosure; Fig 1; 52pp; English.
 XX The cDNA encoding cutinase from amino acid residues 32 to 320 is
 CC especially favoured for the production of cutinase derivatives. It is
 CC operably linked to a promoter such as Ptac and a termination sequence
 CC ,e.g. from Phase fd. A bridging sequence links the truncated cutinase to
 CC the promoter sequences. The bridging sequence is constructed from the
 CC signal sequence naturally associated with F.solan cutinase. Prokaryotic
 CC cells (e.g. E.coli) transformed with the recombinant vector can produce
 CC pure cutinase having higher thermostability than known lipases. See also
 CC AAR06628-R06629. (Updated on 25-MAR-2003 to correct PI field.) (Updated
 CC on 24-OCT-2003 to standardise OS field)
 XX Sequence 1121 BP; 236 A; 320 C; 295 G; 270 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 3, 97e-50 Length: 1121
 Score: 546.00 Matches: 108
 Percent Similarity: 71.1% Conservative: 32
 Best Local Similarity: 54.8% Mismatches: 53
 Query Match: 54.8% Indels: 4
 DB: 2 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x AAQ05859 (1-1121)

QY 1 GlnLeuGly---AlaIleGluAAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
 DB 356 CAGCTTGGTAGAACAACTCCGACGATCTGATCAACGGCAATAGCGTCTCTCGCCGAT 415
 QY 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGly 39
 DB 416 GTCATCTTCATTATTCGCCGAGTTTCAACAGACGGCACTTGGGA---ACTTCGGT 472
 QY 40 ProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleThrIleGlnGly 57
 DB 473 CCTAGCATTCCTCCAACTTGTAGTCCGCTTCGCAAGGACGGTGTCTGATTCAGGCG 532
 QY 58 ValGlyGlyProTyrAspAlaLeuAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGln 77
 DB 533 GTTGGCGGTGCTTACCGAGCACTCTTGGAGACAATGCTCTCCCTCGCGAACCCTCTAGC 592
 QY 78 AlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThr 97
 DB 593 GCGCAATCAGGAGATGTTGTGCTCTTCACAGCGCCCAACACCAAGTCCCTGAGCG 652
 QY 98 ProValValAlaGlyTyrSerGlnGlyValAlaAlaLeuIleAlaAlaValSerGlu 117
 DB 653 ACTTTCATCGCGTGGCTACAGCCAGGGTGTGCTGCTTCGACCGCGCTCCATCGAGGAC 712
 QY 118 LeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsn 137
 DB 713 CTCGACTCGCCATTCGTGACAGATCGCGGAACCTGTTCTGTTCGCTACACCAAGAAC 772
 QY 138 LeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsn 157
 DB 773 CTACGAACCGTGGCGCAATCCCACTACCTCCGCGCAGGACCAAGGCTTCTCGCAAT 832
 QY 158 ValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThr 177

Db 833 ACAGGGGATCTCGTTGTACTGTAGTTCGTTGCTGCACCTCCTTGGCTTATGCT 892
 QY 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
 DB 893 CCTGATGCTCGTGGCCCTGCCCTGAGTTCCTCATCGAGAGAGGTTCGGGCT 943

RESULT 6
 ADH34524
 ID ADH34524 standard; DNA; 2769 BP.
 AC ADH34524;
 XX 11-MAR-2004 (first entry)
 XX Fusarium solani cutinase gene.
 KW Alkanethiol; reactant ligand; substrate; protein chip;
 KW polypeptide immobilisation; enzyme activity; antibody detection;
 KW cutinase; gene; ds.
 OS Fusarium solani.
 PN US2003119054-A1.
 XX 26-JUN-2003.
 XX 07-AUG-2001; 2001US-00923760.
 XX 07-AUG-2001; 2001US-00923760.
 PA (MRKS/) MRKSICH M.
 PA (HODN/) HODNELAND C.
 PI Mrksich M, Hodneland C;
 XX WPI; 2004-080248/08.
 XX New alkanethiols substituted with a reactant ligand useful for
 PT immobilizing polypeptides on gold surfaces, e.g. for determining enzyme
 PT activity or detecting antibodies.
 XX Example 7; SEQ ID NO 5; 57pp; English.
 XX The present invention relates to alkanethiols substituted with a reactant
 CC ligand. Also disclosed is a substrate comprising a surface and a
 CC plurality of moieties on the surface. The moieties are of formula Surf-L-
 CC Q-T where T comprises a reactant ligand, and Surf designates where the
 CC moiety attaches to the surface. The substrate can be incorporated into a
 CC protein chip comprising a substrate bearing the reaction product of a
 CC reactant ligand and a fusion polypeptide comprising a capture polypeptide
 CC corresponding to the reactant ligand. The alkanethiols of the invention
 CC are useful for immobilising polypeptides on gold surfaces, e.g. for
 CC determining enzyme (especially kinase or protease) activity or detecting
 CC antibodies. The present sequence representing the Fusarium solani
 CC cutinase gene is used in the examples of the present invention.
 XX Sequence 2769 BP; 553 A; 745 C; 592 G; 679 T; 0 U; 0 Other;
 SQ

Alignment Scores:
 Pred. No.: 1, 08e-46 Length: 2769
 Score: 519.50 Matches: 107
 Percent Similarity: 65.4% Conservative: 33
 Best Local Similarity: 50.0% Mismatches: 54
 Query Match: 52.2% Indels: 20
 DB: 12 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x ADH34524 (1-2769)

QY 1 GlnLeuGly---AlaIleGluAAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAsp 19
 DB 1051 CAGCTTGGTAGAACAACTCCGACGATCTGATCAACGGCAATAGCGTCTCTCGCCGAT 1110

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QY 20 AlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMet-GlyIle----- 36
Db 1111 GTCATCTTCATTATCCCGAGGTTCAACAGACGCGCAACTGTGTCGTAGAAATTTCT 1170
QY 37 -----ThrValGlyProAlaLeuAl 43
Db 1171 TCTCATGACAACTACTCTTTCTTACACATCCATTAGGGAACCTCTCGTCTCTAGCAATGC 1230
QY 43 aAsnGlyLeuGluSerHisIle-----ArgAsnIleTTPilleGlnGlyValGlyGlyPr 61
Db 1231 CTCACACCTTGTAGTCGCTCGCTCGCAAGGAGCGGTGCTGCAATTCAGGGCGTTGGCGGTGC 1290
QY 61 oTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAs 81
Db 1291 CTACGCAGCACTCTTGGAGACAATGCTCTCCCTCGCGGAACCTCTAGCGCCGCAATCAG 1350
QY 81 pGluGlyLysArgLeuPheAlaLeuAlaAenGlnLysCysProAsnThrProValValAl 101
Db 1351 GGAGATGCTCGGTCTCTTCAGCAGGCCAACACCAAGTGCCTTGACCGGACTTTGATCGC 1410
QY 101 aGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAl 121
Db 1411 CGGTGCTACAGCAGGCTGCTGCACTTGCGCGCGCTCCATCGAGGACCTCGACTCGGC 1470
QY 121 aValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnAr 141
Db 1471 CATTCGTGACAGATCGCCGAACTGTTCTGTTCTGCTACACCAAGAACCTACAGAACCG 1530
QY 141 gGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAl 161
Db 1531 TGCGCGAATCCCACTTACCTCCGACAGGACCAAGGTTCTTGTCAATACAGGGGATCT 1590
QY 161 aValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaAr 181
Db 1591 CGTTTGACTGGTAGCTTGATGCTGCTGCACTCTGCTGCTATGCTGCTGATGCTCG 1650
QY 181 gGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 1651 TGSCCTCGCCCTGAGTTCTCTCATCGAAGGTTGCGGCT 1690

RESULT 7
ADL27534
ID ADL27534 standard; cDNA; 789 BP.
XX
AC ADL27534;
XX
DT 20-MAY-2004 (first entry)
XX
DE cDNA sequence of lipolytic enzyme NBE045.
XX
KW lipolytic enzyme; NBE028; NBE029; NBE030; NBE031; NBE032; NBE033; NBE034;
KW NBE036; NBE038; NBE039; NBE043; NBE045; NBE042; dough; fungal infection;
KW enzyme; ss; gene.
XX
OS Aspergillus niger.
XX
PH Key Location/Qualifiers
FT 1..789
FT /*tag= a
FT /product= "lipolytic enzyme NBE045"
XX
XX W02004018660-A2.
XX
XX 04-MAR-2004.
XX
XX 15-AUG-2003; 2003WO-EP009145.
XX
XX 19-AUG-2002; 2002EP-00102168.
XX 19-AUG-2002; 2002EP-00102169.
XX 19-AUG-2002; 2002EP-00102170.
XX 19-AUG-2002; 2002EP-00102171.
XX 19-AUG-2002; 2002EP-00102172.
XX 19-AUG-2002; 2002EP-00102173.

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PR 19-AUG-2002; 2002EP-00102174.
PR 19-AUG-2002; 2002EP-00102176.
PR 19-AUG-2002; 2002EP-00102178.
PR 19-AUG-2002; 2002EP-00102179.
PR 19-AUG-2002; 2002EP-00102181.
PR 19-AUG-2002; 2002EP-00102183.
XX (STAM ) DSM IP ASSETS BV.
XX
XX Albang R, Folkers U, Fritz A, Gerhard B, Heinrich O;
XX Ilgenfritz H, Maier D, Spreafico F, Wagner C, Boer DL, Meima R;
XX
XX WPI; 2004-226841/21.
XX P-PSDB; ADL27535.
XX
XX Novel lipolytic enzyme, useful for producing dough and/or baked product
XX of dough, and for diagnosis of fungal infections.
XX
XX Claim 7; Page 126-127; 134pp; English.
XX
XX The present sequence encodes a lipolytic enzyme. The specification
XX describes the following lipolytic enzymes: NBE028, NBE029, NBE030,
XX NBE031, NBE032, NBE033, NBE036, NBE038, NBE039, NBE043, NBE045
XX and NBE042. The lipolytic enzymes are useful for producing dough. They
XX are also useful for diagnosis of fungal infections. The enzymes have high
XX specificity towards the substrate, are less antigenic, and produce less
XX undesirable side activities when used in industrial processes and further
XX provide higher yields and low production cost.
XX
XX Sequence 789 BP; 167 A; 220 C; 229 G; 173 T; 0 U; 0 Other;
SQ

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Alignment Scores:

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Pred. No.: 6.26e-46 Length: 789
Score: 506.00 Matches: 101
Percent Similarity: 69.1% Conservative: 33
Best Local Similarity: 52.1% Mismatches: 54
Query Match: 50.8% Indels: 6
DB: 12 Gaps: 3

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US-08-817-997-2_COPY_36_229 (1-194) x ADL27534 (1-789)

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QY 3 GlyAlaIleGluAanGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeu 22
Db 109 GGCTCTACAGCAACGAATCGGATCCGACAAAGTCGCTGCAGGGTGTGCGCGGC 159
QY 23 IlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeu 42
Db 160 ATCTTTGGAGGGGTCACTGAGCTTGGGAATATGGCACCGTAATCGGCCCCCTCTC 219
QY 43 AlaAsnGlyLeuGluSerHisIleArgAsn-----IleTyrIleGlnGlyValGlyGly 60
Db 220 TGCACACACCTGAAATCCAACTCGGATCCGACAAAGTCGCTGCAGGGTGTGCGCGGC 279
QY 61 ProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle 80
Db 280 CAATACACGCGCGGACTCGTGCAGAATCCCTGCCCAAGACACCGATCCGGGGATATC 339
QY 81 AspGluGlyLysArgLeuPheAlaLeuAlaAenGlnLysCysProAsnThrProValVal 100
Db 340 TCCGCGCGAAGCAGATGTTTCAGAGGCGGAATTCGAAGTGTCCCAATACTAAGATTGT 399
QY 101 AlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGly 120
Db 400 CGGGGTGTTATAGTCAAGGAGCGCTGTGATTGACACGCGCTGCAAGAACTCAGCACC 459
QY 121 AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn 140
Db 460 ACCGTGAAAGACCAAGTGAAGGTTGCTGCTCTTCGGGTTTCACGAGAAACGTGAGGAT 519
QY 141 ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp 160
Db 520 CACGGGCAGATCCCTTAATACCTAAGGATGACGTGAAGGTTTATTGTGCCCGTGGCGGAT 579

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FT	sig_peptide	68..160
FT	mat_peptide	/tag= b
FT		161..763
FT		/tag= c
FT		/note= "Claim 22"
XX		
PN	W09741212-A1.	
PD	06-NOV-1997.	
XX		
XX	22-APR-1997;	97WO-DK000179.
PF		
XX	25-APR-1996;	96DK-00000500.
PR	25-APR-1996;	96DK-00000501.
XX		
PA	(NOVO) NOVO-NORDISK AS.	
XX		
PI	Hirayama S, Taira R, Borch K, Sandal T, Halkier T, Oxenboll KM,	
PI	Nielsen B;	
DR	WPI; 1997-549717/50.	
DR	P-PSDB; AAW38264.	
XX		
XX	Lipolytic enzymes useful as detergent additives at high pH - from	
PT	Gliocladium, Verticillium and Trichophaea genera, give good washing	
PT	performance and stability in detergent solutions.	
XX		
PS	Claim 22; Page 43-45; 7lpp; English.	
CC	This DNA sequence from Trichophaea saccata CBS 804.70 includes a coding	
CC	region for a novel lipase (see AAW38264) that has lipolytic activity at	
CC	alkaline pH and which gives good washing performance and stability in	
CC	detergent solutions. The lipase DNA was isolated by cloning a cDNA	
CC	library from T. saccata in a vector, transforming yeast cells, and	
CC	screening by expressed lipolytic activity for positive clones. The	
CC	isolated DNA can be used for recombinant production of the lipase,	
CC	especially the mature enzyme. The DNA is deposited in Escherichia coli	
CC	transformant DSM 11298. Claimed lipases (see also AAW38262 and AAW38263)	
CC	can be used as detergent additives (e.g. as non-dusting granulates,	
CC	stabilised liquids, slurries or protected enzymes) to remove lipid or	
CC	fatty stains, and included with a surfactant in enzymatic detergent	
CC	compositions (claimed) e.g. for laundry and dishwashing, especially at	
CC	high pH. They are also useful for interesterification, total hydrolysis	
CC	of fats and oils and optical isomer resolution. (Updated on 25-MAR-2003	
CC	to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)	
XX		
SQ	Sequence 999 BP; 260 A; 241 C; 239 G; 259 T; 0 U; 0 Other;	
Alignment Scores:		
Pred. No.:	4..44e-45	Length: 999
Score:	499.50	Matches: 96
Percent Similarity:	67.4%	Conservative: 32
Best Local Similarity:	50.5%	Mismatches: 59
Query Match:	50.2%	Indels: 3
DB:	2	Gaps: 2
US-08-817-997-2_COPY_36_229 (1-194) x AAT95846 (1-999)		
Qy	5 IleGluAsnGlyLeuGluSerGlySeraAlaAsnAlaCysProAspAlaIleuLeuPhe 24	
Db	191 GTGGTGATGAACCTGGCAATGC---GGCGGCGGTGTCACAAAGGCCATTCTCATCTTT 247	
Qy	25 AlaArgGlySerThrGluProGlyAnMetGlyIleThrValGlyProAlaLeuAlaAsn 44	
Db	248 GCTAGAGGTACAATGGAGCTGGATAACATGGGGCTTATTAGTCGGGCCAGCTTTCAGGT 307	
Qy	45 GlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrr 62	
Db	308 GGCTTAGAGGCTATGCTGGGTCCAATTAACCTCTGGGTCCAAGGTGTAGTGGCCATAT 367	
Qy	63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlu 82	
b	168 GCTGGCAATCTCCAGGCGCAATCTATTTCAGATGGAAACCTCCCAAAGCCATCCAGGAG 427	

CC proteins, metabolites and biosurfactants particularly alpha-amylase. The
 CC present sequence encodes an A. oryzae plastic-degrading enzyme of the
 CC invention.

SQ Sequence 675 BP; 144 A; 210 C; 174 G; 147 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4.39e-45 Length: 675
 Score: 497.50 Matches: 104
 Percent Similarity: 67.3% Conservative: 28
 Best Local Similarity: 53.1% Mismatches: 57
 Query Match: 49.9% Indels: 7
 DB: 12 Gaps: 4

US-08-817-997-2_COPY_36_229 (1-194) x ADN89479 (1-675)

QY 1 GlnLeuGlyAlaIleGluAsnGlyLeuGluSerAlaAsnAlaCysProAspAla 20
 DB 97 CAGCTCGGTCT---TCCATGACCTCACCAAGGT-----GCATGCAAGGATGTG 144
 QY 21 IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyPro 40
 DB 145 ACCCTCATTTTGGCTCGAGGCTCCCGGAATGGCAACATGGGCACTGTCTATCGGACCC 204
 QY 41 AlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyVal 58
 DB 205 CCTCTCTGCTGCTGCTGAAGCAAGTCCGTCGACAAAGTCTGCTTCCCAAGGTGTG 264
 QY 59 GlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAla 78
 DB 265 GGTGGCTTGTATACAGAGGATGTGCAAAATGCTCTCCCTCAGAACACCCGCCGCCG 324
 QY 79 AsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrPro 98
 DB 325 GCTATCTCCACCGGAAGTCGCTTTTGAACAGCCAGCACCAAGTGGCTTACACCCAG 384
 QY 99 ValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeu 118
 DB 385 ATCGTGGCGGTGGATACAGTCAAGGTAGTGGCGTCTATCGACAAACCGTCCCAACAATC 444
 QY 119 SerGlyAlaValGlyGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeu 138
 DB 445 TCCGCCGAAGTCAAGCAAGGTCAAGGGTGTGTTTCTTCGGCTTCACTCGTAACCTC 504
 QY 139 GlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnVal 158
 DB 505 CAGGACAGGGTCAGATCCCACTACCCCAAGGACAATGTTAAGTCTTTTGTGGGATG 564
 QY 159 GlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIle 178
 DB 565 GGAGATCTTGTCTGGATGGCAGGCTTATGTACCCGCCGCCATTTGACATATACCAT 624
 QY 179 GluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
 DB 625 AATGGG---CCGAGGCTGCTCTTTCCTTCCTTCGTCGAAGGTTCAGTCA 669

RESULT 11

AAT95845

ID AAT95845 standard; DNA; 869 BP.

XX AC

XX AAT95845;

XX 27-AUG-2003 (revised)

XX 25-MAR-2003 (revised)

XX 11-MAY-1998 (first entry)

XX Verticillium lipolytic enzyme DNA.

XX Lipolytic enzyme; lipase; alkalophilic enzyme; detergent; surfactant;

XX esterification; lipid hydrolysis; optical isomer resolution; ss.

XX Verticillium.

Key Location/Qualifiers
 CDS 43..741
 /tag= a
 sig_peptide 43..132
 /tag= b
 mat_peptide 133..738
 /tag= c
 /note= "Claim 22"

W09741212-A1.

06-NOV-1997.

22-APR-1997; 97WO-DK000179.

25-APR-1996; 96DK-00000500.

25-APR-1996; 96DK-00000501.

(NOVO) NOVO-NORDISK AS.

XX Hirayama S, Taira R, Borch K, Sandal T, Halkier T, Oxenboll KM;

XX Nielsen B;

XX WPI; 1997-549717/50.

XX P-PSDB; AAW38263.

XX Lipolytic enzymes useful as detergent additives at high pH - from

XX Gliocladium, Verticillium and Trichophaea genera, give good washing

XX performance and stability in detergent solutions.

XX Claim 22; Page 41-42; 71pp; English.

XX This DNA sequence from Verticillium sp. CBS 830.95 includes a coding
 CC region for a novel lipase (see AAW38263) that has lipolytic activity at
 CC alkaline pH and which gives good washing performance and stability in
 CC detergent solutions. The lipase DNA was isolated by cloning a cDNA
 CC library from the Verticillium sp. in a vector, transforming yeast cells,
 CC and screening by expressed lipolytic activity for positive clones. The
 CC isolated DNA can be used for recombinant production of the lipase,
 CC especially the mature enzyme. The DNA is deposited in Escherichia coli
 CC transformant DSM 10590. Claimed lipases (see also AAW38262 and AAW38264)
 CC can be used as detergent additives (e.g. as non-dusting granulates,
 CC stabilised liquids, slurries or protected enzymes) to remove lipid or
 CC fatty stains, and included with a surfactant in enzymatic detergent
 CC compositions (claimed) e.g. for laundry and dishwashing, especially at
 CC high pH. They are also useful for interesterification, total hydrolysis
 CC of fats and oils and optical isomer resolution. (Updated on 25-MAR-2003
 CC to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 869 BP; 235 A; 194 C; 204 G; 236 T; 0 U; 0 Other;

SQ

Alignment Scores:

Pred. No.: 3.1e-43 Length: 869

Score: 482.00 Matches: 90

Percent Similarity: 68.0% Conservative: 33

Best Local Similarity: 49.7% Mismatches: 56

Query Match: 48.4% Indels: 2

DB: 2 Gaps: 1

US-08-817-997-2_COPY_36_229 (1-194) x AAT95845 (1-869)

QY 16 AlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGly 35

DB 196 GCTTGGCCCCAAGGCTATCTCTTCTCGAGACGATAGACTGATGATGATGGC 255

QY 36 IleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIle 53

DB 256 TTATTGGTTGGCCACCTTTGACACGCTATCTATCGGTATCTTGGGTTCAAAAACCTC 315

QY 54 TrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAlaThrAsnPheLeuProArg 73

DB 316 TGGGTCCCAAGCGTGGGTGGCCATATATGCTGCAAGCTTGGAGGGTAATCTCTTCCGGAT 375

QY 74 GlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLys 93
 DB 376 GGGACCCCTCCTCAAGCCATCCAGGAGATGATTACATTCCTCAATTCGGGATACATAA 435
 QY 94 CysProAsnThrProValValAlaGlyTyrSerGlnGlyValAlaLeuIleAlaAla 113
 DB 436 TGTCCAACTCCAAAGATTGTCACTGGGGATATAGTCAGGTGCTCTCTCGTGGCCGCA 495
 QY 114 AlaValSerGluLeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPheGly 133
 DB 496 GCAATTCGGGATGTCAGGCTTCGATCCGACAGAGATTGTAGGAATGTACTGTTCGGG 555
 QY 134 TyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLys 153
 DB 556 TACTCCAAAACAAACAGAGGACGCTCAGGTAGAGAAACTACTCTAATGACCGACTCCGA 615
 QY 154 ValPheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHis 173
 DB 616 GTTATTGCAACCTGGGATTAAATTGGAGGGACCTTGATTGTTCTGCCAGTGCAC 675
 QY 174 LeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArg 193
 DB 676 CTCCTTATGGAACCAAGCTTCTGCTCTGCTGCAGCACAAATTCCTCGTAGAATCAAT 735
 QY 194 Ala 194
 DB 736 TCT 738
 RESULT 12
 ADN89480
 ID ADN89480 standard; DNA; 780 BP.
 AC ADN89480;
 XX
 DT 29-JUL-2004 (first entry)
 DE A. oryzae plastic-degradation enzyme gene SEQ ID NO:5.
 XX ds; gene; plastic; biosurfactant; alpha-amylase; plastic-degrading;
 KW enzyme.
 XX Aspergillus oryzae.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..780
 FT /tag= a
 FT /product= "plastic-degrading enzyme"
 XX
 PN WO2004038016-A1.
 XX
 PD 06-MAY-2004.
 XX
 PF 17-SEP-2003; 2003WO-JP011861.
 XX
 PR 23-OCT-2002; 2002JP-00308884.
 PR 24-DEC-2002; 2002JP-00371246.
 XX
 XX (TOHO-) TOHOKU TECHNOARCH KK.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PI Abe K, Gomi K, Yamagata Y, Hasegawa F, Maeda H, Nakajima T;
 PI Machida M;
 XX
 DR WPI; 2004-411219/38.
 DR P-PSDB; ADN89487.
 XX
 XX Degradation of (waste) plastics with microorganisms particularly
 PT transformants in presence of biosurfactant, applicable in producing
 PT useful substances like proteins, metabolites and biosurfactants.
 XX
 PS Claim 48; SEQ ID NO 5; 139pp; Japanese.
 XX
 CC The invention relates to a novel method for degrading a plastic in the

CC presence of a biosurfactant using recombinant microorganisms. The method
 CC of the invention is useful for the degradation of (waste) plastics and
 CC also applicable in producing useful substances simultaneously e.g.
 CC proteins, metabolites and biosurfactants particularly alpha-amylase. The
 CC present sequence encodes an A. oryzae plastic-degrading enzyme of the
 CC invention.
 XX
 SQ Sequence 780 BP; 164 A; 230 C; 197 G; 189 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,21e-40 Length: 780
 Score: 455.50 Matches: 95
 Percent Similarity: 65.1% Conservative: 28
 Best Local Similarity: 50.3% Mismatches: 61
 Query Match: 45.7% Indels: 5
 DB: 12 Gaps: 3

US-08-817-997-2_COPY_36_229 (1-194) x ADN89480 (1-780)

QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
 DB 88 AAGAGCTGCGAGATGGCTCT-----TGCAAGCGCATCACCTTCATCTTTGCCCGC 138
 QY 27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
 DB 139 GCTTCCACAGCCAGGACTTTTGGGTATATCAACTGGCCCTGCGAGTCTGCAATGGCTTG 198
 QY 47 Glu---SerHisIleArgAsnIleTyrIleGlnGlyGlyProTyrAspAlaAla 65
 DB 199 AAGATGCCAAAGCGGCCAAGTAGCTTGCAGGGGTGTGGACCAAGTACACGGCAGAC 258
 QY 66 LeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArg 85
 DB 259 CTGCGATCAAAATGCTTTGCCGAGAACACGTCCCAGCTGCCATCCAAAGAGGCACAAGAC 318
 QY 86 LeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSer 105
 DB 319 CTGTTCCAGCAGCGCCGTCACCAAAATGCCCTCACACCAATTTGTGCCGGTGGTATAGC 378
 QY 106 GlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGln 125
 DB 379 CAAGGCACAGCCGTGATGATGATCTCCATCAAGCGTCTACACAGCAACGTGAAGAGAG 438
 QY 126 ValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAla 145
 DB 439 ATCAAGGGTGTGCTCTCTCGGCTACACCCGACGACACAGGAACACGTCAGATTGCC 498
 QY 146 AsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGly 165
 DB 499 AACTTTCCAAAGGACAAGGTCAAGGTCTACTGTCCGTAGCGATATGTTCTGTGACGGC 558
 QY 166 ThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAla 185
 DB 559 ACCTTGATCGTGGGGCCGCCCATTTCACTTAC---CTGGGTAACACCGCGAAGCAACT 615
 QY 186 ArgPheLeuArgAspArgIleArgAla 194
 DB 616 CAGTTCTTGTGTTAAGCTGAGTGCT 642

RESULT 13

ADL27533
 ID ADL27533 standard; DNA; 2371 BP.

XX ADL27533;

AC ADL27533;

XX 20-MAY-2004 (first entry)

DE Genomic sequence of lipolytic enzyme NBE045.

XX lipolytic enzyme; NBE028; NBE029; NBE030; NBE031; NBE032; NBE033; NBE034;
 KW NBE036; NBE038; NBE039; NBE043; NBE045; NBE042; dough; fungal infection;
 KW enzyme; ss.

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2006, 21:53:49 ; Search time 3874 Seconds
(without alignments)
2342.977 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QGATENGLESSANACPD.....SYTIARGEARFLRDIRA 194

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB_spool/US08817997/runat_03022006_161328_18041/app_query.fasta_1
-DB=EST -Qfmt=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blousem62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs04
-USER=US08817997 @CCN 1.1 5315 @runat_03022006_161328_18041 -NCPU=6 -ICPU=3
-NO_MAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	564	56.6	775	8	DR656248
2	564	56.6	790	8	DR650105
3	564	56.6	812	8	DR650176
4	564	56.6	864	8	DR649823
5	564	56.6	873	8	DR653698
6	564	56.6	873	8	DR656249
7	564	56.6	874	8	DR649822

8 564 56.6 874 8 DR653697
9 564 56.6 876 8 DR650104
10 564 56.6 880 8 DR648560
11 564 56.6 880 8 DR656090
12 564 56.6 881 8 DR650471
13 564 56.6 901 8 DR648561
14 564 56.6 905 8 DR650175
15 564 56.6 908 8 DR650470
16 564 56.6 913 8 DR656089
17 564 56.6 924 8 DR646042
18 564 56.6 924 8 DR655065
19 564 56.6 931 8 DR655066
20 511 51.3 672 8 DR646043
21 466 46.8 863 8 DR734519
22 447 44.9 766 6 CF391519
23 405 40.7 602 1 AJ638811
24 309.5 31.1 426 1 AI210810
25 301.5 30.3 479 1 AI210809
26 290.5 29.2 405 1 AI210575
27 284.5 26.6 603 3 BJ292902
28 262 26.3 736 7 CO139663
29 252 25.3 564 3 BM370193
30 241.5 24.2 419 1 AA787593
31 235.5 23.6 565 7 CO140029
32 232 23.3 868 6 CD645681
33 228.5 22.9 702 6 CA284076
34 218.5 21.9 467 6 CF391493
35 216.5 21.7 422 1 AA788247
36 196.5 19.7 704 8 CV950097
37 191 19.2 668 8 CV948750
38 188 18.9 665 8 CV957661
39 185.5 18.6 724 8 CV946800
40 179 18.0 814 7 CO200444
41 170 17.1 393 1 AA966137
42 159.5 16.0 720 7 CO218141
43 156 15.7 377 1 AI211957
44 155.5 15.6 585 8 CV953395
45 153.5 15.4 552 7 CO144719

ALIGNMENTS

RESULT 1

DR656248

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

EST1046365 FvN Gibberella moniliformis cDNA clone FVNB85, mRNA
775 bp linear EST 12-JUL-2005

sequence.

DR656248

GI:70744724

EST.

Gibberella moniliformis

Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Peizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 775)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Unterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAUR

USDA

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncaur.usda.gov

TIGR sequence name: FVNB85TH

Seq primer: AAT TAA CCC TCA AAG GG.

Location/Qualifiers

1..775

/organism="Gibberella moniliformis"

FEATURES

source


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/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNBU85"
/tissue_type="mycelia"
/clone_lib="FVN"

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/note=Vector: pBluescript II SK(+) XR; Site 1: EcoRI; Site 2: XhoI; anamorph: Fusarium verticillioides. Library FVN was obtained from RNA derived from a corn meal medium culture of strain M-3125. These cultures were prepared by inoculating an autoclaved mixture of 25 g corn meal and 5 ml distilled water with 5 ml of water containing 5 x 10⁶ conidia. The inoculated medium was mixed thoroughly, distributed equally into two 100-mm plastic petri dishes, and incubated at room temperature for four or six days."

ORIGIN

Alignment Scores:
 Pred. No.: 8.16e-55 Length: 775
 Score: 564.00 Matches: 109
 Percent Similarity: 71.0% Conservative: 23
 Best Local Similarity: 58.6% Mismatches: 54
 Query Match: 56.6% Indels: 0
 DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR656248 (1-775)

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Qy 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuPheAlaArg 26
Db 184 AATGATATGAGGATGGGATTCCTCGATGTGCCCCCAGCAATTCGATATGCGCGT 243
Qy 27 GlySerThrGluProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db 244 GGTAGACAGAACTGGCACTTGGATCAGGTTGGGCGGATCCTCGCAGAGGCCATG 303
Qy 47 GluSerHisLeuArgAsnLeuTrpIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
Db 304 CAGCTCGCTATCCAGACATCTCGATACAAGGTGTGTGGCGCTATACGGCTGATCTC 363
Qy 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnLeuAspGluGlyLeuArgLeu 86
Db 364 GCGCCCAACTTTCTTCGGGAGGGGACTACTGATGCTCCATGATGAAGCTAAAGGCTG 423
Qy 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db 424 TTCCAAATGGCTTACGATAGTACCCAGATACGCCGCTGTCGACGGCTGGTTATAGTCAA 483
Qy 107 GlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db 484 GGCACGGTTGCTGCGGATATGCATCAGCGAACTTCAAATCGCGCTCCAGAACCGATT 543
Qy 127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyLeuAlaAsn 146
Db 544 GTTGGAGCTCCCTGTTGGATATACCAAGACGAGCAGCTTGGGGCCGCTATTTCGGAAC 603
Qy 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db 604 TATCCTACGGACAAACCAAGATCTTCTGTCGTACGATCTAGTGTGTGACGGAACT 663
Qy 167 LeuLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db 664 TTGTTCACTTCTCTGCTCATTTTCTATACGGTGCAGATGGCGGGTCCAGGTCGCGAA 723
Qy 187 PheLeuArgAspArgIle 192
Db 724 TTCTGTTGGACAGATT 741

```

RESULT 2

DR650105/c
 LOCUS 790 bp mRNA linear EST 12-JUL-2005
 DEFINITION FVN Gibberella moniliformis cDNA clone FVNAR36, mRNA sequence.
 ACCESSION DR650105

VERSION
KEYWORDS
SOURCE
ORGANISM

DR650105.1 GI:70738581

EST.
 Gibberella moniliformis
 Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE
AUTHORS

1 (bases 1 to 790)
 Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
 Uterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
 Kendra,D.F., Town,C.D. and Whitelaw,C.A.

TITLE

Analysis of 87,000 expressed sequence tags reveals alternatively
 spliced introns in multiple genes of the fumonisin gene cluster

JOURNAL

Unpublished (2005)

COMMENT

Contact: Brown, D.W.

USDA/ARS/NCAR

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncar.usda.gov

TIGR sequence name: FVNAR36TV

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

FEATURES
source

1..790
 Location/Qualifiers
 /organism="Gibberella moniliformis"
 /mol_type="mRNA"
 /strain="m3125"
 /db_xref="taxon:117187"
 /clone="FVNAR36"
 /tissue_type="mycelia"
 /clone_lib="FVN"

/note=Vector: pBluescript II SK(+) XR; Site 1: EcoRI;
 Site 2: XhoI; anamorph: Fusarium verticillioides. Library
 FVN was obtained from RNA derived from a corn meal medium
 culture of strain M-3125. These cultures were prepared by
 inoculating an autoclaved mixture of 25 g corn meal and 5
 ml distilled water with 5 ml of water containing 5 x 10⁶
 conidia. The inoculated medium was mixed thoroughly,
 distributed equally into two 100-mm plastic petri dishes,
 and incubated at room temperature for four or six days."

ORIGIN

Alignment Scores:
 Pred. No.: 8.37e-55 Length: 790
 Score: 564.00 Matches: 109
 Percent Similarity: 71.0% Conservative: 23
 Best Local Similarity: 58.6% Mismatches: 54
 Query Match: 56.6% Indels: 0
 DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR650105 (1-790)

```

Qy 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuPheAlaArg 26
Db 712 AATGATATGAGGATGGGATTCCTCCAGTGTGCCCCCAGCAATTCGATATGCGCGT 653
Qy 27 GlySerThrGluProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db 652 GGTAGACAGAACTGGCACTTGGATCAGGTTGGGCGGATCCTCGCAGAGGCCATG 593
Qy 47 GluSerHisLeuArgAsnLeuTrpIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
Db 592 CAGCTCGCTATCCAGACATCTCGATACAAGGTGTGTGGCGCTATACGGCTGATCTC 533
Qy 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnLeuAspGluGlyLysArgLeu 86
Db 532 GCGGCCCAACTTTCTTCGGAGGGGACTACTGATGCTCCATGATGAAGCTAAAGGCTG 473
Qy 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db 472 TTCCAAATGGCTTACGATAGTACCCAGATACGCCGCTGTCGACGGCTGGTTATAGTCAA 413
Qy 107 GlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126

```

```

Db      412  GGACGGTTGTCGTCGGATATGCACTCAGCAACTTCAATCGCGTCCAGAACAGGTT 353
QY      127  LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
Db      352  GTTGGAGTCGCTTGTTCGATATACCAAGAACGAGCAGCTTGGGGCGCGTATTCGGAAC 293
QY      147  TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      292  TATCTTACCGCAAAACCAAGATCTTCTGTCGCTACCGATCTAGTGTGTGACGAAC 233
QY      167  LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db      232  TTGTTCAATCTCTCTGCTCATTTCTATACGGTGCAGATCGCGGCGGTCCAGTCCGGAA 173
QY      187  PheLeuArgAspArgIle 192
Db      172  TTCCTGGTTGGACAGATT 155

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RESULT 3

DR650176/c
LOCUS DR650176 812 bp mRNA linear EST 12-JUL-2005
DEFINITION EST1040293 FvN Gibberella moniliformis cDNA clone FVNAR82, mRNA

ACCESSION DR650176

VERSION DR650176.1 GI:70738652

KEYWORDS EST.

SOURCE Gibberella moniliformis

ORGANISM Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 812)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

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spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAR

1815 N. University St, Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncar.usda.gov

TIGR sequence name: FVNAR82TV

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

Location/Qualifiers

1. 812

/organism="Gibberella moniliformis"

/mol_type="mRNA"

/strain="m3125"

/db_xref="taxon:117187"

/clone="FVNAR82"

/tissue_type="mycelia"

/clone_lib="FvN"

/note="Vector: pBlueScript II SK(+); XR: Site 1: EcoRI;

Site 2: XhoI; anamorph: Fusarium verticillioides. Library

FvN was obtained from RNA derived from a corn meal medium

culture of strain M-3125. These cultures were prepared by

inoculating an autoclaved mixture of 25 g corn meal and 5

ml distilled water with 5 ml of water containing 5 x 10⁶

conidia. The inoculated medium was mixed thoroughly,

distributed equally into two 100-mm plastic petri dishes,

and incubated at room temperature for four or six days."

ORIGIN

Alignment Scores:

Pred. No.: 8,68e-55 Length: 812

Score: 564.00 Matches: 109

Percent Similarity: 71.0% Conservative: 23

Best Local Similarity: 58.6% Mismatches: 54

Query Match: 56.6% Indels: 0

DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR650176 (1-812)

QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
Db 712 AATGATATTGAGGATGGGATTCCTCCAGTTGTCCCCAGCAATCTGATCTATGCGCT 653

QY 27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db 652 GGTAGCAGACAACCTGGCACTTGGATCAGGTTGGCGGATCCTCGCAGAGGCATG 593

QY 47 GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaIleLeu 66
Db 592 CAGTCGCTATCCAGACATCTGGATACAAAGTGTGGTGGCCCTATACGGCTGATCTC 533

QY 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db 532 GCGCCCAACTTCTTCGGAGGGGACTACTGATGCTCCATGATGAAGCTAAAGGCTG 473

QY 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db 472 TTCAAATGGCCTACGATAAGTGCACGATACGCGCTCGTGACGGCTGGTTATAGTCAA 413

QY 107 GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db 412 GGCACGGTGTTCGTCGGATATGCACTCAGCAACTTCAAAATCGCGCTCCAGAACCGGTT 353

QY 127 LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
Db 352 GTTGGAGCTGCTTGTTCGATATACCAAGAACGAGCAGCTTGGGGCGGTATTCGGAAC 293

QY 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db 292 TATCTTACCGCAAAACCAAGATCTTCTGTCGCTACCGATTTAGTGTGTGACGGAAC 233

QY 167 LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db 232 TTGTTCAATCTCTCTGCTCATTTCTATACGGTGCAGATCGCGGCGGTCCAGTCCGGAA 173

QY 187 PheLeuArgAspArgIle 192

Db 172 TTCCTGGTTGGACAGATT 155

RESULT 4

DR649823/c
LOCUS DR649823 864 bp mRNA linear EST 12-JUL-2005
DEFINITION EST1039940 FvN Gibberella moniliformis cDNA clone FVNAP59, mRNA

ACCESSION DR649823

VERSION DR649823.1 GI:70738298

KEYWORDS EST.

SOURCE Gibberella moniliformis

ORGANISM Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 864)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAR

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Fax: 309 681 6689

Email: brown@ncar.usda.gov

TIGR sequence name: FVNAP59TV

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

Location/Qualifiers

1. 864

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source
1. .864
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNAP59"
/tissue_type="mycelia"
/clone_lib="FVN"
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNAP59"
/tissue_type="mycelia"
/clone_lib="FVN"
Note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
conidia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."

ORIGIN
Alignment Scores:
Pred. No.: 9,44e-55 Length: 864
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservativeness: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR649823 (1-864)

Qy 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuPheAlaArg 26
Db 690 AATGATATTGGAGTGGGATTTCTCCAGTTGTCTCCCGCAGCAATTTCTGATCGCGT 631

Qy 27 GlySerThrGluProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db 630 GGTAGCACAGAACTGGCAACCTTGGAAATCACGGTTGGGCCCATCTTCGACAGCGCATG 571

Qy 47 GluSerHisIleArgAsnIleTrrIleGlnGlyValGlyProAlaLeuAlaAsnGlyLeu 66
Db 570 CAGCTCGCTATCCAGACATCTGGATACAGGTGTGTGGGCCCATCTTCGACAGCGCATG 571

Qy 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db 510 GCGCCCAACTTTCTCCGAGGGGAGTACTGATGCTCCATTTGATGAAGCTAAAGGCTG 451

Qy 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyLysSerGln 106
Db 450 TTCCAAATGGCTTACGATAGTCCAGATACAGCGCTGTCGACGGCTGGTTATAGTCAA 391

Qy 107 GlyAlaAlaLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db 390 GGCACGGTGTCTCGGATATGCACTACGCACTTCAATCGCTCCAGAACCGATT 331

Qy 127 LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyLysIleAlaAsn 146
Db 330 GTTGGAGCTGCTTGTGGATATACCAAGACGAGCAGCTTGGGGCGGTATTCGGAAC 271

Qy 147 TyrProArgGluThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db 270 TATCTCTACGACAAACCAAGATCTTCTGCTCTGCTACGGAATCTAGTGTGTGACGGAAC 211

Qy 167 LeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db 210 TTGTTCTATCTCTCTATTTTCTATACGGTGCAGATGCGGCGGTCCAGTCCGGA 151

Qy 187 PheLeuArgAspArgIle 192
Db 150 TTCTTGTGGACAGATT 133

RESULT 5
DR653698/c
LOCUS
DEFINITION RST1043815 FVN Gibberella moniliformis cDNA clone FVNBE45, mRNA
sequence.
DR653698 1 GI:70742174
EST.
Gibberella moniliformis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 873)
Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.
Uterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
Kendrick,D.F., Town,C.D. and Whitelaw,C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
USDA
1315 N. University St, Peoria, IL 61604, USA
Tel: 309 681 6230
Fax: 309 681 6689
Email: brownw@ncaur.usda.gov
TIGR sequence name: FVNBE45TV
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES
Location/Qualifiers
1..873
/organism="Gibberella moniliformis"
/mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
/clone="FVNBE45"
/tissue_type="mycelia"
/clone_lib="FVN"
/notes="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhoI; anamorph: Fusarium verticillioides. Library
FVN was obtained from RNA derived from a corn meal medium
culture of strain M-3125. These cultures were prepared by
inoculating an autoclaved mixture of 25 g corn meal and 5
ml distilled water with 5 ml of water containing 5 x 10e7
conidia. The inoculated medium was mixed thoroughly,
distributed equally into two 100-mm plastic petri dishes,
and incubated at room temperature for four or six days."

ORIGIN
Alignment Scores:
Pred. No.: 9,57e-55 Length: 873
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservativeness: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR653698 (1-873)

Qy 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuPheAlaArg 26
Db 690 AATGATATTGGAGTGGGATTTCTCCAGTTGTCTCCCGCAGCAATTTCTGATCTATGCGCGT 631

Qy 27 GlySerThrGluProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db 630 GGTAGCACAGAACTGGCAACCTTGGAAATCACGGTTGGGCCCATCTTCGACAGCGCATG 571

Qy 47 GluSerHisIleArgAsnIleTrrIleGlnGlyValGlyProAlaLeuAlaAsnGlyLeu 66
Db 570 CAGCTCGCTATCCAGACATCTGGATACAGGTGTGTGGGCCCATCTTCGACAGCGCATG 571

Qy 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db 510 GCGCCCAACTTTCTCCGAGGGGAGTACTGATGCTCCATTTGATGAAGCTAAAGGCTG 451

Qy 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyLysSerGln 106
Db 450 TTCCAAATGGCTTACGATAGTCCAGATACAGCGCTGTCGACGGCTGGTTATAGTCAA 391

Qy 107 GlyAlaAlaLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db 390 GGCACGGTGTCTCGGATATGCACTACGCACTTCAATCGCTCCAGAACCGATT 331

Qy 127 LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyLysIleAlaAsn 146
Db 330 GTTGGAGCTGCTTGTGGATATACCAAGACGAGCAGCTTGGGGCGGTATTCGGAAC 271

Qy 147 TyrProArgGluThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db 270 TATCTCTACGACAAACCAAGATCTTCTGCTCTGCTACGGAATCTAGTGTGTGACGGAAC 211

Qy 167 LeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db 210 TTGTTCTATCTCTCTATTTTCTATACGGTGCAGATGCGGCGGTCCAGTCCGGA 151

Qy 187 PheLeuArgAspArgIle 192
Db 150 TTCTTGTGGACAGATT 133

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RESULT 5
DR653698
LOCUS
DEFINITION

QY 107 GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
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 Db 390 GGACCGTTGTCGTCGGATGATCAGCGAACTTCAAATCGCCGTCAGAACCCAGGTT 331
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 330 GTTGGAGCTGCTCTGTTGGATATACCAAGACGACGCTTGGGGCGGTATCCGAAC 271
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 270 TATCTACGACAAACCAAGATCTTCTGTCCTACGATCTAGTGTGTGACGAAC 211
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 167 LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 210 TTGTTCAATCTTCTGCTCATTTTCTATACGGTGCAGATCGCGGGTCCAGGTCCGGAA 151
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 187 PheLeuArgAspArgIle 192
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 150 TTCCTGGTTGGACAGATT 133

RESULT 6

DR656249/c
 LOCUS DR656249 873 bp mRNA linear EST 12-JUL-2005
 DEFINITION EST1046366 FVN Gibberella moniliformis cDNA clone FVNB085, mRNA

ACCESSION

VERSION DR656249.1 GI:70744725

KEYWORDS

EST.

SOURCE

Gibberella moniliformis

ORGANISM

Gibberella moniliformis

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 873)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAR

USDA

1815 N. University St., Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncar.usda.gov

TIGR sequence name: FVNB085TV

Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

Location/Qualifiers

1..873

/organism="Gibberella moniliformis"

/mol_type="mRNA"

/strain="m3125"

/db_xref="taxon:117187"

/clone="FVNB085"

/tissue_type="mycelia"

/clone_lib="FVN"

/note="Vector: pBlueScript II SK(+), Site 1: EcoRI;

Site 2: XhoI; anamorph: Fusarium verticillioides. Library

FVN was obtained from RNA derived from a corn meal medium

culture of strain M-3125. These cultures were prepared by

inoculating an autoclaved mixture of 25 g corn meal and 5

ml distilled water with 5 ml of water containing 5 x 10⁶

conidia. The inoculated medium was mixed thoroughly,

distributed equally into two 100-mm plastic petri dishes,

and incubated at room temperature for four or six days."

ORIGIN

Alignment Scores:

Pred. No.: 9.57e-55 Length: 873

Score: 564.00 Matches: 109

Percent Similarity: 71.0% Conservative: 23

Best Local Similarity: 58.6% Mismatches: 54
 Query Match: 56.6% Indels: 0
 DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR656249 (1-873)

QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 690 AATGATATTGAGGATGGGATTCTCCAGTTGTCCCCAGCAANTTCTGATCTATGCGGT 631
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 630 GTAGACACAGACTGGCACTTGGATCAGGTTGGGCCGATCTCCGAGAGCCATG 571
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 47 GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 570 CAGCTCGCTATCCAGACATCTGGATACAGGTTGTTGGGCCCTATACGGCTGATCTC 511
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 510 GCGCCCAACTTCTTCGGAGGGGACTACTGATGCTCCATTCATGATGAAGCTAAAGGCTG 451
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaIleGlyTyrSerGln 106
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 450 TTCAAATGGCTACGATAGTGCCTCCAGATACGCCGTCGACGGCTGTTATAGTCAA 391
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 QY 107 GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 390 GGCACGGTTGTCGTCGGATATGCACTCAGCGAACTTCAAATCGCCGTCAGAACCCAGGTT 331
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 QY 127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 330 GTTGGAGCTGCTCTGTTGGATATACCAAGAACGAGCAGCTTGGGGCGGTATTCGGAAC 271
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 270 TATCTACGACAAACCAAGATCTTCTGTCCTACGATCTAGTGTGTGACGAAC 211
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 167 LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 210 TTGTTCAATCTTCTGCTCATTTTCTATACGGTGCAGATCGCGGGTCCAGGTCCGGAA 151
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 QY 187 PheLeuArgAspArgIle 192
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 150 TTCCTGGTTGGACAGATT 133

RESULT 7

DR649822

LOCUS

DEFINITION

DR649822

VERSION

DR649822.1

GI:70738297

KEYWORDS

EST.

SOURCE

Gibberella moniliformis

Gibberella moniliformis

ORGANISM

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

1 (bases 1 to 874)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

Kendra, D.F., Town, C.D. and Whitelaw, C.A.

Analysis of 87,000 expressed sequence tags reveals alternatively

spliced introns in multiple genes of the fumonisin gene cluster

Unpublished (2005)

Contact: Brown, D.W.

USDA/ARS/NCAR

USDA

1815 N. University St., Peoria, IL 61604, USA

Tel: 309 681 6230

Fax: 309 681 6689

Email: brown@ncar.usda.gov

TIGR sequence name: FVNB085TV

```

LOCUS       DR653697               874 bp    mRNA    linear    EST 12-JUL-2005
DEFINITION   EST1043814 FvN Gibberella moniliformis cDNA clone FVNBE45, mRNA
sequence.
ACCESSION   DR653697
VERSION     DR653697.1
KEYWORDS    GI:70742173
SOURCE      Gibberella moniliformis
ORGANISM    Gibberella moniliformis
REFERENCE   1 (bases 1 to 874)
AUTHORS     Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.,
            Uterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
            Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE       Analysis of 87,000 expressed sequence tags reveals alternatively
            spliced introns in multiple genes of the fumonisin gene cluster
            Unpublished (2005)
JOURNAL     Unpublished (2005)
COMMENT     Contact: Brown, D.W.
            USDA/ARS/NCAR
            USDA
            1815 N. University St, Peoria, IL 61604, USA
            Tel: 309 681 6230
            Fax: 309 681 6689
            Email: brown@ncar.usda.gov
            TIGR sequence name: FVNBE45TH
            Seq primer: AAT TAA CCC TCA CTA AAG GG.
            Location/Qualifiers
                source          1..874
                    /organism="Gibberella moniliformis"
                    /mol_type="mRNA"
                    /strain="m3125"
                    /db_xref="taxon:117187"
                    /clone="FVNBE45"
                    /tissue_type="mycelia"
                    /clone_lib="FvN"
                    /notes="Vector: pBlueScript II SK(+/-) XR; Site 1: EcoRI;
                    Site 2: XhoI; anamorph: Fusarium verticillioides. Library
                    FvN was obtained from RNA derived from a corn meal medium
                    culture of strain M-3125. These cultures were prepared by
                    inoculating an autoclaved mixture of 25 g corn meal and 5
                    ml distilled water with 5 ml of water containing 5 x 10e7
                    conidia. The inoculated medium was mixed thoroughly
                    distributed equally into two 100-mm plastic petri dishes,
                    and incubated at room temperature for four or six days."

ORIGIN
Alignment Scores:
Pred. No.:      9.58e-55      Length:      874
Score:          564.00      Matches:    109
Percent Similarity: 71.0%      Conservative: 23
Best Local Similarity: 58.6%      Mismatches: 54
Query Match:    56.6%      Indels:     0
DB:             8           Gaps:       0

US-08-817-997-2_COPY_36_229 (1-194) x DR649822 (1-874)
QY      7  AsnglyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
DB      184  AATGATATTGAGGATGGGATTCCTCCAGTTGTCCCCAGCAATTCTGATCTATGCGGT 243
QY      27  GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
DB      244  GGTAGCACAGAACCTGGCAACCTTGAATCAGCGTTGGGCGCATCTCGCAGAGGCCATG 303
QY      47  GluSerHisIleArgAsnIleTrrIleGlnGlyValGlyGlyProThrAspAlaLeu 66
DB      304  CAGCTCGCTATCCAGACATCTGGATACAGGTTGGTGGGCGCCATATACGGCTGATCTC 363
QY      67  AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
DB      364  GGCCCAACTTCTTCGGGAGGGGATCTACTGATCGCTCCATTGATGAGCTAAAGGCTG 423
QY      87  PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyThrSerGln 106
DB      424  TTCCAATGGCTTACGATAAGTCCAGATACGCGCGTGTGACGGCTGGTTATAGTCAA 483
QY      107  GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
DB      484  GGCACGGTTGTCTCGATATGACATCAGCAACTTCAAAATCCGCGCTCCAGAACCCAGTT 543
QY      127  LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
DB      544  GTTGGAGCTGCCCTTGTGGATATACAGAACGACGAGCTTGGGGCGGTATTCGGAAC 603
QY      147  TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
DB      604  TATCTTACGGACAAAACCAAGATCTTCTGTCTCGCTACGGATCTAGTGTGTGACGGAAC 663
QY      167  LeuIleIleThrProAlaHisLeuSerThrIleGluAlaArgGlyGluAlaAlaArg 186
DB      664  TTGTTCATTCTTCTCTCTATTTCTATACGGTGCAGATCGCGCGGTCCAGGTCCCGAA 723
QY      187  PheLeuArgAspArgIle 192
DB      724  TTCCTGGTGGACAGATT 741

RESULT 8
DR653697

```

```

Db      424 TTCCAAATGGCTTACGATAGTGCCAGATACGCCGCTGCTGACGGTGGTTATAGTCAA 483
Qy      107 GlyAlaAlaLeuAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db      484 GGCACGGTTGTCGTCGATATGCACTCAGCGAACTTCAAAATCGCCGTCAGAACCCAGGTT 543
Qy      127 LysGlyValAlaLeuPheGlyThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
Db      544 GTTGGAGTCGCTTGTGATATACCAAGACGAGCAGCTTGGGGCCGATTTCCGAAC 603
Qy      147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      604 TATCTTACGACAAACCAAGATCTTCTGTCTGCTACGATCTAGTGTGACGAACT 663
Qy      167 LeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db      664 TTGTTTATCTTCTGCTCATTTTCTATACGGTGACAGATCGCGGGTCCAGGTCCGGAA 723
Qy      187 PheLeuArgAspArgIle 192
Db      724 TTCCTGGTTGGACAGATT 741

```

RESULT 9

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DR650104          876 bp  mRNA  linear  EST 12-JUL-2005
LOCUS             EST1040221 FVN Gibberella moniliformis cDNA clone FVNAR36, mRNA
DEFINITION

```

ACCESSION

```
DR650104

```

VERSION

```
DR650104.1 GI:70738580

```

KEYWORDS

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EST.

```

SOURCE

```
Gibberella moniliformis

```

ORGANISM

```

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 876)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,
Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,
Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR

```

REFERENCE

```
1815 N. University St., Peoria, IL 61604, USA

```

```
1815 N. University St., Peoria, IL 61604, USA

```

```
Tel: 309 681 6230

```

```
Fax: 309 681 6689

```

```
Email: brown@ncaur.usda.gov

```

```
TIGR sequence name: FVNAR36TH

```

```
Seq primer: AAT TAA CCC TCA AAG GG.

```

FEATURES

```
Location/Qualifiers

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1..876

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/organism="Gibberella moniliformis"

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/mol_type="mRNA"

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/strain="m3125"

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/db_xref="taxon:117187"

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/clone="FVNAR36"

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/tissue_type="mycelia"

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/clone_lib="FVN"

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```
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;

```

```
Site 2: XhoI; anamorph: Fusarium verticillioides. Library

```

```
FVN was obtained from RNA derived from a corn meal medium

```

```
culture of strain M-3125. These cultures were prepared by

```

```
inoculating an autoclaved mixture of 25 g corn meal and 5

```

```
ml distilled water with 5 ml of water containing 5 x 106

```

```
conidia. The inoculated medium was mixed thoroughly,

```

```
distributed equally into two 100-mm plastic petri dishes,

```

```
and incubated at room temperature for four or six days."

```

ORIGIN

```
1815 N. University St., Peoria, IL 61604, USA

```

```
Alignment Scores:

```

```
Pred. No.:

```

```

Score: 564.00  Matches: 109
Percent Similarity: 71.0%  Conservative: 23
Best Local Similarity: 58.6%  Mismatches: 54
Query Match: 56.6%  Indels: 0
DB: 8  Gaps: 0

```

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US-08-817-997-2_copy_36_229 (1-194) x DR650104 (1-876)
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Qy      7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg 26
Db      204 AATGATATTGAGGATGGGATTCCTCCAGTTGTGCCCCAGCAATTTCTGATCTATGCGCT 263
Qy      27 GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db      264 GGTAGCAGACAGACCTGGCACTTGGATACAGGTGTGGGCCGATCCTCGAGAGCCATG 323
Qy      47 GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeu 66
Db      324 CAGCTCGCTATCCAGACATCTGGATACAGGTGTGGTGGGCCCTATACGCTGATCTC 383
Qy      67 AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db      384 GCGCCCAACTTCTTCCGGAGGGGACTACTGATGCCTCCATTGATGAAGCTAAAGGCTG 443
Qy      87 PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db      444 TTCCAATGGCTTACGATAGTGCCAGATACGCCGCTGTCGACGGCTGGTTATAGTCAA 503
Qy      107 GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db      504 GGCACGGTTGTCGTCGATATGCACTCAGCGAACTTCAATCGCCGCTCAGAACACAGTT 563
Qy      127 LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsn 146
Db      564 GTTGGAGTCGCTTGTGATATACCAAGACGAGCAGCTTGGGGCCGCTATTCCGAAC 623
Qy      147 TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      624 TATCTTACGACAAACCAAGATCTTCTGTCTGCTACGATCTAGTGTGTCGACGAACT 683
Qy      167 LeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db      684 TTGTTTATCTTCTGCTCATTTTCTATACGGTGACAGATCGCGGGTCCAGGTCCGGAA 743
Qy      187 PheLeuArgAspArgIle 192
Db      744 TTCCTGGTTGGACAGATT 761

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RESULT 10

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DR648560

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```
LOCUS

```

```
DEFINITION

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sequence.

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DR648560

```

```
VERSION

```

```
DR648560.1 GI:70737035

```

```
KEYWORDS

```

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EST.

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```
SOURCE

```

```
ORGANISM

```

```
Gibberella moniliformis

```

```
Gibberella moniliformis

```

```
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

```

```
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

```

```
1 (bases 1 to 880)

```

```
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,

```

```
Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,

```

```
Kendra, D.F., Town, C.D. and Whitelaw, C.A.

```

```
Analysis of 87,000 expressed sequence tags reveals alternatively

```

```
spliced introns in multiple genes of the fumonisin gene cluster

```

```
Unpublished (2005)

```

```
Contact: Brown, D.W.

```

```
USDA/ARS/NCAUR

```

```
USDA

```

```
1815 N. University St., Peoria, IL 61604, USA

```

```

9.61e-55  Length: 876

```


Qy	87	PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln	106
Db	472	TTCCAAATGCGCTACGATAAGTGCACAGATACGCCCGCTGTCGACGGCTGGTTATAGTCAA	413
Qy	107	GlyAlaAlaLeuLeuAlaAlaValSerGlnLeuSerGlyAlaValLysGluGlnVal	126
Db	412	GGACAGGTTGCTGCGGATATGCACTCAGCGAACTTCAAAATCGCGCTCCAGAACCAAGGTT	353
Qy	127	LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyLeuAlaAsn	146
Db	352	GTGAGAGCTGCTTGTGATATACCAAGAACGAGCAGCTTGGGGCCGATATCCGAAAC	293
Qy	147	TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr	166
Db	292	TATCCTACGGACAAACCAAGATCTTCTGCTGCTACCGATCTAGTGTGTGACGGAAT	233
Qy	167	LeuLeuLeuThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg	186
Db	232	TTGTTTCATTCTCTGCTCATTTTCTATACGGTCAGATGCGCGGGTCCAGGTCGCGAA	173
Qy	187	PheLeuArgAspArgIle	192
Db	172	TTCTGTTGGACAGATT	155
RESULT 12			
LOCUS	DR650471/c		
DEFINITION	DR650471	881 bp	linear EST 12-JUL-2005
ACCESSION	DR650471	EST1040388	PvN Gibberella moniliformis cDNA clone FVNAT77, mRNA
VERSION	DR650471.1	GI:70738947	
KEYWORDS	EST.		
SOURCE	Gibberella moniliformis		
ORGANISM	Gibberella moniliformis		
REFERENCE	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
AUTHORS	Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.		
TITLE	1 (bases 1 to 881)		
JOURNAL	Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y.,		
COMMENT	Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D.,		
	Kendra, D.F., Town, C.D. and Whitelaw, C.A.		
	Analysis of 87,000 expressed sequence tags reveals alternatively		
	spliced introns in multiple genes of the fumonisin gene cluster		
	unpublished (2005)		
	Contact: Brown, D.W.		
	USDA/ARS/NCAR		
	1815 N. University St, Peoria, IL 61604, USA		
	Tel: 309 681 6230		
	Fax: 309 681 6689		
	Email: brown@ncar.usda.gov		
	TIGR sequence name: FVNAT77V		
	Seq primer: GTA ATA CGA CTC ACT ATA GGG C.		
FEATURES	Location/Qualifiers		
source	1..881		
	/organism="Gibberella moniliformis"		
	/mol_type="mRNA"		
	/strain="m3125"		
	/db_xref="taxon:117187"		
	/clone="FVNAT77"		
	/tissue_type="mycelia"		
	/clone_lib="FVN"		
	/notes="Vector: pBlueScript II SK(+); XR; Site 1: EcoRI;		
	Site 2: XhoI; anamorph: Fusarium verticillioides. Library		
	FVN was obtained from RNA derived from a corn meal medium		
	culture of strain M-3125. These cultures were prepared by		
	inoculating an autoclaved mixture of 25 g corn meal and 5		
	ml distilled water with 5 ml of water containing 5 x 10 ⁶		
	conidia. The inoculated medium was mixed thoroughly,		
	distributed equally into two 100-mm plastic petri dishes,		
	and incubated at room temperature for four or six days."		

Alignment Scores:
Pred. No.: 9,69e-55 Length: 881
Score: 564.00 Matches: 109
Percent Similarity: 71.0% Conservative: 23
Best Local Similarity: 58.6% Mismatches: 54
Query Match: 56.6% Indels: 0
DB: 8 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x DR650471 (1-881)

Qy	7	AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArg	26
Db	712	AATGATATTGAGGATGGGGATTCCTCCCAATTTGTCCCCCAGCAATTTGTATCTATGCGCGT	653
Qy	27	GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu	46
Db	652	GGTAGCACAGAACCTGGCAACCTTGGAAATACGGTTGGGCCGATCCTCCAGAGGCCATG	593
Qy	47	GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeu	66
Db	592	CAGCTCGCTATCCAGACATCTGGATACAGGTGTTGGTGGCCCTATACGGCTGATCTC	533
Qy	67	AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu	86
Db	532	CGGCCCAACTTCTTCCGGAGGGACTACTGATGCTCCATTGATGAAGCTAAAAAGCTG	473
Qy	87	PheAlaLeuAlaAsnGlnIleCysProAsnThrProValValAlaGlyClyTyrSerGln	106
Db	472	TTCCAAATGGCTTACGATAAGTGCCAGATACGCCCGCTGTGACGGCTGTTATAGTCAA	413
Qy	107	GlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal	126
Db	412	GGCACGGTTGTCGTCGGATATGCACTCAGCGAATCTTCAATCGCCGTCAGAACCCAGGTT	353
Qy	127	LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyClyIleAlaAsn	146
Db	352	GTTGGAGCTGCTTGTGTTGGATATACCAAGAACGAGCAGCTTTGGGGGGCGTATTCGGAAC	293
Qy	147	TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr	166
Db	292	TATCCTACGGACAAACCAAGATCTTCTGTCTGCTACGGATTTAGTGTGTGACCGAATC	233
Qy	167	LeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg	186
Db	232	TTGTTCAATCTCTGCTCAATTTCTATACGGTGCAGATCGCGGGTCCAGGTCGGAA	173
Qy	187	PheLeuArgAspArgIle	192
Db	172	TTCTGTTGGACAGATT	155

RESULT 13
DR648561/c
LOCUS EST1038678 FVN Gibberella moniliformis cDNA clone FVNAH48, mRNA
DEFINITION sequence.
ACCESSION DR648561
VERSION DR648561.1 GI:70737036
KEYWORDS Gibberella moniliformis
SOURCE Gibberella moniliformis
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 901)
AUTHORS Brown,D.W., Chung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.
Uterback,T., Smith,S., Feldblum,T., Glenn,A.E., Plattner,R.D.,
Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE Analysis of 87,000 expressed sequence tags reveals alternatively
spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL Unpublished (2005)
COMMENT Contact: Brown, D.W.
USDA/ARS/NCAR
1815 N. University St, Peoria, IL 61604, USA

ORIGIN


```

Db      378  GCGCCCACTTTCTTCGGAGGGGACTACTGATGCTCCATTGATGAAGCTAAAGGCTG 437
Qy      87  PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db      438  TTCCAAAATGGCTACGATAGTCCAGATACGCCCGCTGCGAGCGGTGGTTATAGTCAA 497
Qy      107  GlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db      498  GGCACGGTTGTCGTGGATGATGACCTCAGCAACTTCAAAATCGCCGTCAGAACACCGATT 557
Qy      127  LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyLeuAlaAsn 146
Db      558  GTTGGAGCTGCTTGTGGATATACCAAGACGAGCGCTTGGGGCCGCTATTCGGAAC 617
Qy      147  TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      618  TATCTCTACGACAAACCAAGATCTTCTGCTGCTACGAGTCTAGTGTGTGACGGAAC 677
Qy      167  LeuLeuLeuThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArg 186
Db      678  TTGTTCAATTCCTGCTCATTTTCTATACGGTGCAGATCGCGGGTCCAGGTCCGGAA 737
Qy      187  PheLeuArgAspArgile 192
Db      738  TTCTCTGGTTGGACAGATT 755

RESULT 15
LOCUS   DR650470
DEFINITION 908 bp mRNA linear EST 12-JUL-2005
VERSION 1
KEYWORDS  DR650470.1 GI:70738946
SOURCE   Gibberella moniliformis
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
          Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 908)
AUTHORS  Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L., Lee,Y.,
          Utterback,T., Smith,S., Feldblyum,T., Glenn,A.E., Plattner,R.D.,
          Kendra,D.F., Town,C.D. and Whitelaw,C.A.
TITLE     Analysis of 87,000 expressed sequence tags reveals alternatively
          spliced introns in multiple genes of the fumonisin gene cluster
JOURNAL   Unpublished (2005)
COMMENT   Contact: Brown, D.W.
          USDA/ARS/NCAR
          1815 N. University St, Peoria, IL 61604, USA
          Tel: 309 681 6230
          Fax: 309 681 6689
          Email: brown@ncar.usda.gov
          TIGR sequence name: FVNAT77TH
          Seq primer: AAT TAA CCC TCA CTA AAG GG.
FEATURES
         Location/Qualifiers
         1..908
         /organism="Gibberella moniliformis"
         /mol_type="mRNA"
         /strain="m3125"
         /db_xref="taxon:117187"
         /clone="FVNAT77"
         /tissue_type="mycelia"
         /clone_lib="FVN"
         /note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
         Site 2: XhoI; anamorph: Fusarium verticillioides. Library
         FVN was obtained from RNA derived from a corn meal medium
         culture of strain M-3125. These cultures were prepared by
         inoculating an autoclaved mixture of 25 g corn meal and 5
         ml distilled water with 5 ml of water containing 5 x 107
         conidia. The inoculated medium was mixed thoroughly,
         distributed equally into two 100-mm plastic petri dishes,
         and incubated at room temperature for four or six days."

```

```

ORIGIN
Alignment Scores: 1.01e-54 Length: 908
Pred. No.: 564.00 Matches: 109
Score: 71.0% Conservative: 23
Percent Similarity: 58.6% Mismatches: 54
Best Local Similarity: 56.6% Indels: 0
Query Match: 8 Gaps: 0
DB: 8

US-08-817-997-2_COPY_36_229 (1-194) x DR650470 (1-908)

Qy      7  AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleuIlePheAlaArg 26
Db      198  AATGATATTGAGGATGGGATTCCTCCAGTTGTCCCCCAGCAATTCGTATCTATGCGCGT 257
Qy      27  GlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeu 46
Db      258  GGTAGCAGACAGACTTGGCAACTTGGATACAGGTGGGGCCGATCTTCGACAGAGCCATG 317
Qy      47  GluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeu 66
Db      318  CAGTCGCTATCCAGACATCTGGATACAAGTGTGGTGGGCCCTATACGGCTGATCTC 377
Qy      67  AlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeu 86
Db      378  GCGCCCAACTTTCTTCGGAGGGGACTACTGATGCTCCATTCATGAAGCTAAAGGCTG 437
Qy      87  PheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGln 106
Db      438  TTCCAAAATGGCTACGATAGTGGCCAGATACGCCCGCTGCGAGCGGTGTTATAGTCAA 497
Qy      107  GlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnVal 126
Db      498  GGCACGGTTGTCGTGGATATGCACTCAGCAACTTCAAAATCGCCGTCAGAACACCGATT 557
Qy      127  LysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyLeuAlaAsn 146
Db      558  GTTGGAGCTGCTTGTGGATATACCAAGAACAGCAGACTTGGGGCCGCTATTCGGAAC 617
Qy      147  TyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThr 166
Db      618  TATCTCTACGACAAACCAAGATCTTCTGCTGCTGCTACGAGTCTAGTGTGTGACGGAAC 677
Qy      167  LeuLeuLeuThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGlyGluAlaAlaArg 186
Db      678  TTGTTCAATTCCTGCTCATTTTCTATACGGTGCAGATCGCGGGTCCAGGTCCGGAA 737
Qy      187  PheLeuArgAspArgile 192
Db      738  TTCTCTGGTTGGACAGATT 755

Search completed: February 5, 2006, 00:19:11
Job time : 3878 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

QM protein - nucleic search, using frame_plus_p2n model

Run on: February 4, 2006, 22:50:57 ; Search time 161 Seconds
(without alignments)
2141.907 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QUGATENGLESGSANACPD.....SYTIERGEARFLDRIRA 194

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q-/abs/ABSWEB_spool/US08817997/runat_03022006_161330_18065/app_query.fasta_1
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-HOST=abs06p -USER=US08817997 @CGN 1.1.290 @runat_03022006_161330_18065
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-WARN TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	991	99.5	994	2	US-08-817-997A-1
2	500.5	50.3	914	3	US-09-177-234-2
3	499.5	50.2	999	3	US-09-177-234-7
4	482	48.4	869	3	US-09-177-234-5
5	260	26.1	768	3	US-10-231-478-2
6	260	26.1	798	3	US-09-585-468-2
7	260	26.1	798	3	US-10-114-115A-2
8	260	26.1	798	3	US-10-114-116-2
9	260	26.1	798	3	US-09-999-170-1

10	189.5	19.0	651	3	US-09-894-844-13	Sequence 13, Appli
11	189.5	19.0	1054	3	US-09-050-739-9	Sequence 9, Appli
12	189.5	19.0	15239	2	US-08-390-878-17	Sequence 17, Appli
c 13	189.5	19.0	4403765	3	US-09-103-840A-2	Sequence 1, Appli
c 14	189.5	19.0	4411529	3	US-09-103-840A-1	Sequence 2, Appli
15	188.5	18.9	1060	3	US-09-050-739-13	Sequence 13, Appli
16	188.5	18.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
17	188.5	18.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
18	178	17.9	800	3	US-09-050-739-51	Sequence 51, Appli
19	167.5	16.8	950	3	US-09-050-739-55	Sequence 55, Appli
20	130	13.1	1125	2	US-08-997-080-153	Sequence 153, App
21	130	13.1	1125	2	US-08-997-362-153	Sequence 153, App
22	130	13.1	1125	3	US-09-095-855-153	Sequence 153, App
23	130	13.1	1125	3	US-09-324-542-153	Sequence 153, App
24	130	13.1	1125	3	US-09-205-426-153	Sequence 153, App
25	120.5	12.1	470	3	US-09-060-756-157	Sequence 157, App
26	120.5	12.1	470	3	US-09-670-314-157	Sequence 157, App
27	112	11.2	503	2	US-08-997-080-111	Sequence 111, App
28	112	11.2	503	2	US-08-997-362-111	Sequence 111, App
29	112	11.2	503	3	US-09-095-855-111	Sequence 111, App
30	112	11.2	503	3	US-09-324-542-111	Sequence 111, App
31	112	11.2	503	3	US-09-205-426-111	Sequence 111, App
32	108	10.8	87	3	US-09-873-075A-5	Sequence 5, Appli
33	106	10.6	57	3	US-09-007-288E-86	Sequence 86, Appli
34	98	9.8	287	3	US-09-533-559-1362	Sequence 1362, Ap
c 35	97	9.7	11029	3	US-09-902-540-1004	Sequence 1004, Ap
c 36	91	9.1	420	3	US-09-060-756-496	Sequence 496, App
37	91	9.1	420	3	US-09-670-314-496	Sequence 496, App
c 38	91	9.1	601	3	US-09-949-016-181597	Sequence 181597,
c 39	91	9.1	601	3	US-09-949-016-181598	Sequence 181598,
c 40	89.5	9.0	125672	3	US-09-949-016-16956	Sequence 16956, A
c 41	88	8.8	2163	3	US-09-252-991A-5310	Sequence 5310, A
c 42	88	8.8	3282	3	US-09-252-991A-5256	Sequence 5256, Ap
c 43	88	8.8	4158	3	US-09-252-991A-5348	Sequence 5348, Ap
c 44	88	8.8	4953	3	US-09-252-991A-5227	Sequence 5227, Ap
c 45	88	8.8	4953	3	US-09-252-991A-5227	Sequence 5227, Ap

ALIGNMENTS

RESULT 1

US-08-817-997A-1
; Sequence 1, Application US/08817997A
; Patent No. 5827719
; GENERAL INFORMATION:
; APPLICANT: Sandal, Thomas
; APPLICANT: Kauppinen, Sakari
; APPLICANT: Kofod, Lene V.
; TITLE OF INVENTION: An Enzyme With Lipolytic
; TITLE OF INVENTION: Activity
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 58277190 No. 5827719disk Of No. 5827719th America, Inc.
; STREET: 405 Lexington Avenue - 64th Fl.
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,997A
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 7435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4316.204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-878-9652

TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 43..729
OTHER INFORMATION:
US-08-817-997A-1

Alignment Scores:
Pred. No.: 2,69e-105 Length: 994
Score: 991.00 Matches: 193
Percent Similarity: 99.5% Conservative: 0
Best Local Similarity: 99.5% Mismatches: 1
Query Match: 99.5% Indels: 0
DB: 2 Gaps: 0

US-08-817-997-2_COPY_36_229 (1-194) x US-08-817-997A-1 (1-994)

QY 1 GlnLeuGlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAla 20
DB 148 CAGCTGGAGCCATCGAGAACGGCTTGAGAGCGGCGAGCGCCAAACGCTGCCCGCAGCGC 207
QY 21 IleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyPro 40
DB 208 ATCTGATCTTTGCTCGCGCTCGAGCGAGCGCAACATGGGCATCACCGTCGGCCCT 267
QY 41 AlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrpIleGlnGlyValGlyGly 60
DB 268 GCTCTGCCCAACGGCTTGAGTCCCATCCGGAACATCTGGATCCAGGGCGTCGGCGGC 327
QY 61 ProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle 80
DB 328 CCTTACGAGCGCGCTGGCCACCAACTTCTCGCGGGGCGACCTCGCAGGCGCAACATC 387
QY 81 AspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValVal 100
DB 388 GACGAGGGCAAGCGCTGTTTGGCTGGCCCAACAAAGTGCCTCAACACGCGCGCTCGTC 447
QY 101 AlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGly 120
DB 448 GCCGGGGGTACAGCCAGGGCGGCGGCTCATCGCTGCCCGCGTCAGCGAGCTCAGCGGC 507
QY 121 AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsn 140
DB 508 GCCGTCAAGGAGCAGGTCAAGGGCGTGCCTCTTCGATACACCCAAACCTCCAGAAC 567
QY 141 ArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAsp 160
DB 568 CGTGGCGCATCCCAACTACCGCGGAGCGACCAAGGTGTTCTGCAACGTTGGCGAC 627
QY 161 AlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAla 180
DB 628 GCGGTCTGCACCGGACGCTCATCATCACCCCGCGCATCTGTGTCATACGATCAGGCG 687
QY 181 ArgGlyGluAlaAlaArgPheLeuArgAspArgIleArgAla 194
DB 688 CGCGGTGAGCCCGGAGGTTCCTGCGGGATCGCATCCGTGCT 729

RESULT 2

US-09-177-234-2
Sequence 2, Application US/09177234A
Patent No. 6350604
GENERAL INFORMATION:
APPLICANT: Hirayama, Satoshi
APPLICANT: Taira, Rikako
APPLICANT: Borch, Kim
APPLICANT: Sandal, Thomas

APPLICANT: Halkier, Torben
APPLICANT: Oxendoll, Karen M.
APPLICANT: Nielsen, Bjarne R.
TITLE OF INVENTION: Alkaline Lipolytic Enzyme
FILE REFERENCE: 4698.204-US
CURRENT APPLICATION NUMBER: US/09/177,234A
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: 500/96
EARLIER FILING DATE: 1996-04-25
EARLIER APPLICATION NUMBER: 501/96
EARLIER FILING DATE: 1996-04-25
EARLIER APPLICATION NUMBER: PCT/DK97/00179
EARLIER FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 914
TYPE: DNA
ORGANISM: Gliocladium sp.
FEATURE:
NAME/KEY: CDS
LOCATION: (21)...(713)
NAME/KEY: mat_peptide
LOCATION: (114)...(713)
NAME/KEY: sig_peptide
LOCATION: (21)...(113)
US-09-177-234-2

Alignment Scores:
Pred. No.: 1,62e-48 Length: 914
Score: 500.50 Matches: 95
Percent Similarity: 67.9% Conservative: 34
Best Local Similarity: 50.0% Mismatches: 58
Query Match: 50.3% Indels: 3
DB: 2 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x US-09-177-234-2 (1-914)

QY 5 IleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuPhe 24
DB 144 GTGCGTGACGAGCTGGCAATGCG---GGCAGCGCGTCCCCCAAGGCCATTCTCATCTTT 200
QY 25 AlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsn 44
DB 201 GCTCGAGCACAAATGGAGCTGGATAACATGGCTTATTGGTCGGCGCAGCTCTTGCAAGT 260
QY 45 GlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyr 62
DB 261 GGCTTAGAGGCGATCTTGGGTTGCAACACCTCTGGGTCAAGGGGTGGGTGCCCATAT 320
QY 63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlu 82
DB 321 GCCGCCAACCTTGAGGGCAATCTATTTCAGATGGAACACCTCTTAAGCCATCCAGGAG 380
QY 83 GlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 102
DB 381 ATGCTTAGCTGCTCCCAATTGGCGGACACCAAGTCCCAAACTTAAGATTGTACAGGG 440
QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
DB 441 GGTATATAGCAAGGTGCTGCATCTGTCGCGCTGCTATTTCGCGATGTCAAGGCTTCATT 500
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
DB 501 CGACAAAGATTGCGGAAACCGTACTCTTTGGGTATCTATAAAACAAACAGAGGAACGA 560
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
DB 561 CAGGTAGAAACTACTCAACTGATCGGCTCGGGTTTACTGTAACTCTCGAGACTTGATT 620
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
DB 621 TGTGAAGGACCTTGATTGTTTCTACCACACATCTTCTTTATGGAGTCCAGGCTGCTGTT 680

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QY 183 GLuAlaAlaArgPheLeuArgAspArgile 192
Db 681 CGAGTGCCTCCAGTTCCTCGCCACAGATC 710
RESULT 3
US-09-177-234-7
; Sequence 7, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Trichophaea saccata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (68)...(763)
; NAME/KEY: mat peptide
; LOCATION: (161)...(763)
; NAME/KEY: sig peptide
; LOCATION: (68)...(160)
US-09-177-234-7
Alignment Scores:
Pred. No.: 2.4e-48 Length: 999
Score: 499.50 Matches: 96
Percent Similarity: 67.4% Conservative: 32
Best Local Similarity: 50.5% Mismatches: 59
Query Match: 50.2% Indels: 3
DB: 3 Gaps: 2
US-08-817-997-2_COPY_36_229 (1-194) x US-09-177-234-7 (1-999)
QY 5 IleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePhe 24
Db 191 GTGCGTGAAGTCAATGCGCAATGCG---GGCGGCGCGTGTCCCAAGGCCATTTCTCATCTTT 247
QY 25 AlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsn 44
Db 248 GCTAGAGGTACATGATGCGTGTATATAGTCGGGCCAGCTCTTGCAGGT 307
QY 45 GlyLeuGluSerHisIle-----ArgAsnIleTrrIleGlnGlyValGlyGlyProTyr 62
Db 308 GGCCTAGAGGTATGCTGGGTTCAATATACCTCTGGGTCCAGGTGTAGGTGGCCAATAT 367
QY 63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlu 82
Db 368 GCTGCCAATCTCGAGGCCAATCTATTTCAGATGGAAACACCTCCCAAGGCCATCCAGGAG 427
QY 83 GlyLysArgLeuPheAlaAlaAsnGlnLysCysProAsnThrProValValAlaGly 102
Db 428 ATGCTTAGTCTGCTCCAAATTAGGGGACCAAGTGTCCAAACTCTAAGATTGTACAGGG 487
QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaAlaValSerGluLeuSerGlyAlaVal 122
Db 488 GGGTATAGCCCAAGGCGCTGCACTGCTATTTCGCGACGTCAAGGCTTCCATT 547
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
Db 548 CGACAAAAGATTGTAGGAACCTGTACTCTTTGGGTACACCAAAAACAAACAGAAACGGA 607
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db 608 CAGGTAGAAAACCTACTCAACTGATCGACTCCGGGTATTATCGAACCGCGGAGACTTGATT 667
QY 163 CysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
Db 668 TGTCAAGGACCTTGATTGTCTCCAGCGCATTTCTTTACGGAGATCAGGCTGCTGCT 727
QY 183 GLuAlaAlaArgPheLeuArgAspArgile 192
Db 728 CCAGCAGCCCGAGTTCCTTGCCAGCAAGATC 757
RESULT 4
US-09-177-234-5
; Sequence 5, Application US/09177234A
; Patent No. 6350604
; GENERAL INFORMATION:
; APPLICANT: Hirayama, Satoshi
; APPLICANT: Taira, Rikako
; APPLICANT: Borch, Kim
; APPLICANT: Sandal, Thomas
; APPLICANT: Halkier, Torben
; APPLICANT: Oxenboll, Karen M.
; APPLICANT: Nielsen, Bjarne R.
; TITLE OF INVENTION: Alkaline Lipolytic Enzyme
; FILE REFERENCE: 4698.204-US
; CURRENT APPLICATION NUMBER: US/09/177,234A
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: 500/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: 501/96
; EARLIER FILING DATE: 1996-04-25
; EARLIER APPLICATION NUMBER: PCT/DK97/00179
; EARLIER FILING DATE: 1997-04-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 869
; TYPE: DNA
; ORGANISM: Verticillium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43)...(738)
; NAME/KEY: mat peptide
; LOCATION: (133)...(738)
; NAME/KEY: sig peptide
; LOCATION: (43)...(132)
US-09-177-234-5
Alignment Scores:
Pred. No.: 2.1e-46 Length: 869
Score: 482.00 Matches: 90
Percent Similarity: 68.0% Conservative: 33
Best Local Similarity: 49.7% Mismatches: 56
Query Match: 48.4% Indels: 2
DB: 3 Gaps: 1
US-08-817-997-2_COPY_36_229 (1-194) x US-09-177-234-5 (1-869)
QY 16 AlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGluProGlyAsnMetGly 35
Db 196 GCTTGCCCAAGGCTATCTCTCTCTTGTCTCGAGAACGATAGACTTGATACATGGGC 255
QY 36 IleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIle 53
Db 256 TTATTGGTTGGGCGACCTCTTGCAGCGGTCTATCGGGGTATCTTGGGTTCAAAAAACCTC 315
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QY	54	TpIleGInGlyValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuProArg	73
Db	316	TGGGTCCAAGCGTGGGTGGCCAATATGCTCAAGCTTGGAGGGTAATCTCTTTCCGGAT	375
QY	74	GlyThrSerGlnAlaAsnIleAspGluGlyIysArgLeuPheAlaLeuAlaAsnGlnLys	93
Db	376	GGGACCCCTCTCAAGCCATCCAGGAGATGATTACATTGCTCAATTGGCGGGATCTAA	435
QY	94	CysProAsnThrProValValAlaGlyGlyTyrsSerGlnGlyAlaAlaLeuIleAlaAla	113
Db	436	TGTCCAAACTCCAGATTGTCACTGGGGATATAGTCAAGTGCTGCTCTGTGGCCGCA	495
QY	114	AlaValSerGluLeuSerGlyAlaValIysGluGlnValLysGlyValAlaLeuPheGly	133
Db	496	GCAATTCCGGATGTCAAGCTTCGATCCGACAGAAGATTGTAGGAACGTGTACTGTTCCGG	555
QY	134	TyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrrProArgGluArgThrLys	153
Db	556	TACTCCAAAAACAAACAGAGGAACGGTCAGGTAGAAAACTACTCTAATGACCGACTCCGA	615
QY	154	ValPheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHis	173
Db	616	GTTTATTGCAACCTGGGGATTAAATTTCGAGGGGACCTTGATTGTTCTGCCCATGTGCAC	675
QY	174	LeuSerTyrrThrIleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIleArg	193
Db	676	CTCTCTTATGGAAACCAAGCTTCTGGTCTCTGCAGCACAATTCCTCGCTAGTAGAATCAAT	735
QY	194	Ala 194	
Db	736	TCT 738	

```

RESULT 5
US-10-231-478-2
; Sequence 2, Application US/10231478
; Patent No. 6936445
; GENERAL INFORMATION:
; APPLICANT: KAWABE, TOMOYASU
; APPLICANT: KAWATAMARI, MASASHI
; TITLE OF INVENTION: ENZYME PREPARATION AND METHOD OF USING THE SAME
; FILE REFERENCE: 7372/73243
; CURRENT APPLICATION NUMBER: US/10/231,478
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: JP 2001-365495
; PRIOR FILING DATE: 2001-09-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(765)
US-10-231-478-2

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Alignment Scores:		
Pred. No.:	9,286-21	768
Score:	260.00	62
Percent Similarity:	50.5%	Conservative: 30
Best Local Similarity:	34.1%	Mismatches: 70
Query Match:	26.1%	Indels: 20
DB:	3	Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-231-478-2 (1-768)

Qy	11	SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaAaGlySerThrGlu	30
Db	229	AlaGAlrTTACTGGTGCCCTGCAGGATTACACGGTCTCTTCGCCCGGAAACAGTGAG	288
Qy	31	ProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle	50

289	CCGGAAACGTTGGTGCTCGTCGGACCTCTTGTCTGAGGCGTTTGAGGAGCCGTC	348	
Qy	51	-----ArgAsnIleThrIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAlaThr	68
Db	349	GGTGGCGTCCGCTTGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG	402
Qy	69	AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLyAsArgLeuPheAla	88
Db	403	GGATATTGGCTGGAGT-----GAGCGCGTGGCAGCAAGGCA	441
Qy	89	LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly	102
Db	442	ATGCATCTCAGGCCAGCGACATTCTCTCCAAGTGTCCGCACACCAAGCTTGTCTAGT	501
Qy	103	GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal	122
Db	502	GGCTATTCCAGGGCTCCGATGTTTCACAATGCCGTGAGCACTTCTCGCGGAACAC	561
Qy	123	LysGluGlnValIysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly	142
Db	562	GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAAGGGCAAG	612
Qy	143	GlyIleAlaIleThrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal	162
Db	613	GCTCTCCCAACAGTTGATGCTTCCGGGTCCACACTGTGTGTCACCGCTGGAGACACTATT	672
Qy	163	CysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly	182
Db	673	TGCAGAACAGCGTATTATTCTGCCCGCTCACTTGACTACGCTGTGTGATGTGCTTCT	732
Qy	183	GluAla	184
Db	733	CGCGCT	738

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RESULT 6
US-09-585-468-2
; Sequence 2, Application US/09585468
; Patent No. 6537790
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Co. Ltd.
; TITLE OF INVENTION: Esterase Genes and Use thereof
; FILE REFERENCE: P150409
; CURRENT APPLICATION NUMBER: US/09/585,468
; CURRENT FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (768)
; US-09-585-468-2

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Alignment Scores:					
Pred. No.:	9.8e-21	Length:	798		
Score:	260.00	Matches:	62		
Percent Similarity:	50.1%	Conservative:	30		
Best Local Similarity:	34.5%	Mismatches:	70		
Query Match:	26.1%	Indels:	20		
DB:	3	Gaps:	6		

US-08-817-997-2_COPY_36_229 (1-194) x US-09-585-468-2 (1-798)

Qy 11 SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGlu 30
 :::| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 229 AATGGATTACTGTGCTGCCTGCACCGATTACACCGTTCCTCCGCCGCGGAACCAAGTGAG 288

Qy 31 ProGlyAsnMetGlyIleThrValcIyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
 ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 289 CCCGGAAACGTGTGTGTCCTCGTCCGACCTCCTCTTGCTAGGCGCTTTGAGGGAGCCGNC 348

Qy 51 -----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAlaThr 68

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Db      349  GGTGCGTCCGCTTGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402
QY      69  AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
Db      403  GGATATTGGCTGGAGGT-----GAAGCCGCTGGCAGCAAGGCA 441
QY      89  LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
Db      442  ATGGCATCTCAGGCCAGGACATTCTCTCAAGTGTCCGACCAACAGCTTGTATGAGT 501
QY      103  GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
Db      502  GGCTATTCCAGGGCTGCCAGATTGTTCAATGCCGTTGAGCAACTCTCTCGGGAACAC 561
QY      123  LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
Db      562  GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAAGGGCAAG 612
QY      143  GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db      613  GCTCTCCCAACAGTTGATGCTTCCCGCGTCCACACTGTGTGCCAGCTGGAGACACTATT 672
QY      163  CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
Db      673  TGGAGAACAGCGTTATTATTGCGCGCTCACTTGACCTACCGCTGTGATGGCTTCT 732

QY      183  GluAla 184
Db      733  GCGGCT 738

```

RESULT 7

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US-10-114-115A-2
; Sequence 2, Application US/10114115A
; Patent No. 6812008
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Co. Ltd.
; TITLE OF INVENTION: Esterase Genes and Use thereof
; FILE REFERENCE: P150409
; CURRENT APPLICATION NUMBER: US/10/114,115A
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/585,468
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
US-10-114-115A-2

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Alignment Scores:
Pred. No.: 9.8e-21      Length: 798
Score: 260.00          Matches: 62
Percent Similarity: 50.5%      Conservative: 30
Best Local Similarity: 34.1%   Mismatches: 70
Query Match: 26.1%           Indels: 20
DB: 3                     Gaps: 6

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US-08-817-997-2_COPY_36_229 (1-194) x US-10-114-115A-2 (1-798)

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QY      11  SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGlu 30
Db      229  AATGATTTACTGGTCCGCGCAGGATTACACCGTTCTCTCCCGCGGAACCGTAG 288
QY      31  ProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
Db      289  CCGGAACGTTGGTGTCTCTGGACCTCTCTTGTGAGCGCTTGGAGGAGCGGTC 348
QY      51  -----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAlaThr 68
Db      349  GGTGCGTCCGCTTACGTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402

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Db      349  GGTGCGTCCGCTTGAGCTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402
QY      69  AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
Db      403  GGATATTGGCTGGAGGT-----GAAGCCGCTGGCAGCAAGGCA 441
QY      89  LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
Db      442  ATGGCATCTCAGGCCAGGACATTCTCTCAAGTGTCCGACCAACAGCTTGTATGAGT 501
QY      103  GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
Db      502  GGCTATTCCAGGGCTGCCAGATTGTTCAATGCCGTTGAGCAACTCTCTCGGGAACAC 561
QY      123  LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
Db      562  GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAAGGGCAAG 612
QY      143  GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db      613  GCTCTCCCAACAGTTGATGCTTCCCGCGTCCACACTGTGTGCCAGCTGGAGACACTATT 672
QY      163  CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
Db      673  TGGAGAACAGCGTTATTATTGCGCGCTCACTTGACCTACCGCTGTGATGGCTTCT 732

QY      183  GluAla 184
Db      733  GCGGCT 738

RESULT 8
US-10-114-116-2
; Sequence 2, Application US/10114116
; Patent No. 6828129
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Co. Ltd.
; TITLE OF INVENTION: Esterase Genes and Use thereof
; FILE REFERENCE: P150409
; CURRENT APPLICATION NUMBER: US/10/114,116
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US/09/585,468
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
US-10-114-116-2

Alignment Scores:
Pred. No.: 9.8e-21      Length: 798
Score: 260.00          Matches: 62
Percent Similarity: 50.5%      Conservative: 30
Best Local Similarity: 34.1%   Mismatches: 70
Query Match: 26.1%           Indels: 20
DB: 3                     Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-114-116-2 (1-798)

QY      11  SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGlu 30
Db      229  AATGATTTACTGGTCCGCGCAGGATTACACCGTTCTCTTCGCGCGGAACCGTAG 288
QY      31  ProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
Db      289  CCGGAACGTTGGTGTCTCTGGACCTCTCTTGTGAGCGCTTGGAGGAGCGGTC 348
QY      51  -----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAlaThr 68
Db      349  GGTGCGTCCGCTTACGTTCCAGGGTGTCAACGGC---TATTCTGCATCTGTC---GAG 402

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QY 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
Db 403 GGATATTGGCTGGAGT-----GAGCGCGTGGCAGCAAGGCA 441
QY 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
Db 442 ATGGCATCTCAGGCCAGCGACATTCTCCAAAGTGTCCGACACCAAGCTTGTGATGAGT 501
QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
Db 502 GGTATTCCAGGGCTGCCAGATGTTCAATGCCGTGGACAACTTCTCGCGGAACAC 561
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
Db 562 GCAAGCAAGATCAGCAGCGTCTCTCTTTTCGGA-----GACCCATCAAGGGCAAG 612
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db 613 GCTCTCCCAACGTTGATGCTTCCCGCTCCACACTGTGTGCCACGCTGGAGACACTATT 672
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
Db 673 TGCAGAACAGCGTTATTATTCTGCCGCTCCTTACCTGACCTACGCTGTGATGGCTTCT 732
QY 183 GluAla 184
Db 733 GCGGCT 738
RESULT 9
US-09-999-170-1
; Sequence 1, Application US/09999170
; Patent No. 6869791
; GENERAL INFORMATION:
; APPLICANT: KAWABE, TOMOYASU
; APPLICANT: KISHIMOTO HIRAMINE, KAE
; TITLE OF INVENTION: METHOD FOR STERILIZING TRANSFORMED CELLS
; FILE REFERENCE: 7372/72243
; CURRENT APPLICATION NUMBER: US/09/999,170
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: JP 2000-368180
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 798
; TYPE: DNA
; ORGANISM: ASPERGILLUS FLAVUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(768)
US-09-999-170-1
Alignment Scores:
Pred. No.: 9,8e-21 Length: 798
Score: 260.00 Matches: 62
Percent Similarity: 50.5% Conservative: 30
Best Local Similarity: 34.1% Mismatches: 70
Query Match: 26.1% Indels: 20
DB: 3 Gaps: 6
US-08-817-997-2_COPY_36_229 (1-194) x US-09-999-170-1 (1-798)
QY 11 SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySerThrGlu 30
Db 229 AATGGATTTACTGGTGCCTGCACGGATTACACCGTTCTTTCGCCCGCAACAGTGAG 288
QY 31 ProGlyAsnMetGlyThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
Db 289 CCCGGAACCGTGGTGTCTTCGCGACCTCTCTTCTGAGCGGTTTGAGGAGCGCGTC 348
QY 51 -----ArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAlaThr 68
Db 519 -----GAGCGTGGTGGCGGCTTCTGCTGACCTCGCTTACC 192
Db 349 GGTGGCTGCCCTTGAGCTTCCAGGGTGTCAAGGCG---TATTCTGCATCTGTCTC---GAG 402
QY 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
Db 403 GGATATTGGCTGGAGT-----GAGCGCGTGGCAGCAAGGCA 441
QY 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
Db 442 ATGGCATCTCAGGCCAGCGACATTCTCCAAAGTGTCCGACACCAAGCTTGTGATGAGT 501
QY 103 GlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
Db 502 GGTATTCCAGGGCTGCCAGATGTTCAATGCCGTGGACAACTTCTCGCGGAACAC 561
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
Db 562 GCAAGCAAGATCAGCAGCGTCTCTCTTTTCGGA-----GACCCATCAAGGGCAAG 612
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db 613 GCTCTCCCAACGTTGATGCTTCCCGCTCCACACTGTGTGCCACGCTGGAGACACTATT 672
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
Db 673 TGCAGAACAGCGTTATTATTCTGCCGCTCCTTACCTGACCTACGCTGTGATGGCTTCT 732
QY 183 GluAla 184
Db 733 GCGGCT 738
RESULT 10
US-09-894-844-13
; Sequence 13, Application US/09894844
; Patent No. 6686166
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-13
Alignment Scores:
Pred. No.: 1,08e-12 Length: 651
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservative: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 3 Gaps: 7
US-08-817-997-2_COPY_36_229 (1-194) x US-09-894-844-13 (1-651)
QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
Db 76 GCGCGTGTGCGCGCATCGGATCGGTGTTCCGACATCGCGTCTGTTTCTCGCGCGC 135
QY 28 SerThrGluProGlyAsnMetGlyThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
Db 136 ACGCATCAGGCTTCTGCTCTTGGC---GACGTGCGTGGCGGCTTCTGCTGACCTCGCTTACC 192
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QY 48 SerHisIleArgAsnIleTrrIleGlnGlyValGlyGlyProTyrAspAlaLeuAla 67
 Db 193 TCGCAA-----GTTGGCGGGCGGTGCGATTGGGGTCTACGCG 228
 QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
 Db 229 GTGACTACCCAGCAGCAGCTACCGCGCGAGCGGTCAACCGGTTCCGATGATGCG 288
 QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
 Db 289 AGCGCCACATCCAGCGCAGCGTCCGCGAGCTGCCGGAACACAGGATTGTGTGGTGGC 348
 QY 104 TyrSerGlnGlyAlaLeuAlaValSerGluLeuSerGlyAlaValLys 123
 Db 349 TATTCCGAGGTTCCGCGGTTCGATTTGTCCACCTCCGCGATGCCCGCGGTGGCA 408
 QY 124 GlnGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
 Db 409 GATCATGTCCCGCTGTGCGCCCTTTTCGGCGAGCCATCCAGTGTCTCCAGCATGTTG 468
 QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
 Db 469 TGGGGCGGGGTCGTTGCCGACATCGGTCCGCTGTATAGCTCTAAGACCATAACTTG 528
 QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
 Db 529 TGTGCTCCGACGATCAATATGACCGAGGCGGCAATATTATG---GGCATGTTTCG 585
 QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
 Db 586 TATGTTCACTCGGGGATGACAGCCAGGCGGACATTCGCGCGAACAGGCTC 639

RESULT 11

US-09-050-739-9
 ; Sequence 9, Application US/09050739
 ; Patent No. 6641814
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDERSEN, Peter
 ; APPLICANT: NIELSEN, Rikke
 ; APPLICANT: OETTINGER, Thomas
 ; APPLICANT: RASMUSSEN, Peter Birk
 ; APPLICANT: ROSENKRANDS, Ida
 ; APPLICANT: WELDRINGH, Karin
 ; APPLICANT: FLORIO, Walter
 ; TITLE OF INVENTION: NUCLEIC ACIDS FRAGMENTS AND POLYPEPTIDE FRAGMENTS
 ; TITLE OF INVENTION: DERIVED FROM M. TUBERCULOSIS

FILE REFERENCE: 670001-2002.1
 ; CURRENT APPLICATION NUMBER: US/09/050,739
 ; EARLIER FILING DATE: 1998-03-30
 ; EARLIER APPLICATION NUMBER: 0376/97
 ; EARLIER FILING DATE: 1997-04-02
 ; EARLIER APPLICATION NUMBER: 1277/97
 ; EARLIER FILING DATE: 1997-11-10
 ; EARLIER APPLICATION NUMBER: 60/044,624
 ; EARLIER FILING DATE: 1997-04-18
 ; EARLIER APPLICATION NUMBER: 60/070,488
 ; EARLIER FILING DATE: 1998-01-05
 ; NUMBER OF SEQ ID NOS: 173
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9

LENGTH: 1054
 TYPE: DNA

ORGANISM: Mycobacterium tuberculosis
 US-09-050-739-9

Alignment Scores:
 Pred. No.: 2,14e-12 Length: 1054
 Score: 189.50 Matches: 61
 Percent Similarity: 43.4% Conservatives: 25
 Best Local Similarity: 30.8% Mismatches: 89
 Query Match: 19.0% Indels: 23
 DB: 3 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-09-050-739-9 (1-1054)
 QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
 Db 276 GGCGGTGTGCGCGCATCGGATCCGTGTTCGGACATCGCGGTGCTTTTCGCTCGCGGC 335
 QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
 Db 336 ACGCATCAGGCTCTTGGTCTTGGC---GACGTGCGGTGAGCGGTTCGTGCTACGCTGCTAC 392
 QY 48 SerHisIleArgAsnIleTrrIleGlnGlyValGlyGlyProTyrAspAlaLeuAla 67
 Db 393 TCGCAA-----GTTGGCGGGCGGTTCGATTGGGGTCTACGCG 428
 QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
 Db 429 GTGAATACCCAGCAGCAGCTACCGCGCGAGCGGTCAACCGTTCGATGATGCG 488
 QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
 Db 489 AGCGCCACATCCAGCGCAGCGTCCGCGAGCTGCCGGAACACAGGATTGTGTGCTGCTGGC 548
 QY 104 TyrSerGlnGlyAlaLeuIleAlaValSerGluLeuSerGlyAlaValLys 123
 Db 549 TATTCCGAGGTTCCGCGGTTCGATTTGTCCACCTCCGCGATGCCCGCGGTGGCA 608
 QY 124 GlnGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
 Db 609 GATCATGTCCGCGGTGTGCGCCCTTTTCGGCGAGCCATCCAGTGGTTCCTCCAGCATGTTG 668
 QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
 Db 669 TGGGGCGGGGTCGTTGCCGACATCGGTCCGCTGTATAGCTCTAAGACCATAACTTG 728
 QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
 Db 729 TGTGCTCCGACGATCCAATATGACCGAGGCGGCAATATTATG---GCGCATGTTTCG 785
 QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
 Db 786 TATGTTCACTCGGGGATGACAGCCAGGCGGACATTCGCGCGGCGAACAGGCTC 839

RESULT 12

US-08-390-878-17
 ; Sequence 17, Application US/08390878
 ; Patent No. 5700683
 ; GENERAL INFORMATION:
 ; APPLICANT: Stover, Charles K.
 ; APPLICANT: Mahairas, Gregory G.
 ; TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
 ; STREET: One Market Plaza, Steuart Street Tower, 20th
 ; STREET: Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/390,878
 ; FILING DATE: 17-FEB-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom
 ; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 15371A-17

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/543/9600
TELEFAX: 415/543/5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15239 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-390-878-17

Alignment Scores:
Pred. No.: 9,24e-11 15239
Score: 189.50 61
Percent Similarity: 43.4% 25
Best Local Similarity: 30.8% 89
Query Match: 19.0% 23
DB: 2 7

US-08-817-997-2_COPY_36_229 (1-194) x US-08-390-878-17 (1-15239)

QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGly 27
DB 6642 GCGGTCGTGCGCGCATCGGATCCGTGTCGACATCCGCGTCGTTTCGCTCGCGC 6701
QY 28 SerThrGluProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 6702 AGCATCAGGCTTCGCTTGGC---GAGTCGGTGAGCGTTCGTCGACTCGCTTACC 6758
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAla 67
DB 6759 TCGCAA-----GTTGGCGGCGGTCGATTCGGGTCCTACGCG 6794
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
DB 6795 GTGAACATACCCAGCAGCAGCTACCGCGGAGCGCGTCAACGGTTCCGATGATCG 6854
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
DB 6855 AGCGCCACATCAGCGGACCGTCGCGCAGCTGCCCGAACAACAGGATGTGCTGTGGC 6914
QY 104 TyrSerGlnGlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLys 123
DB 6915 TATTCGAGGTGCGAGCGTCATCGATTGTCACCTCGCGGATCGCGCGGCGGCA 6974
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 6975 GATCATGTCCGCGCTGTCGCCCTTTTCGCGAGCCATCCAGTGGTTTCTCCAGCATGTTG 7034
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 7035 TGGGCGCGGCGGTGCTGCGCAATCGGTCCGCTGTATAGCTCTAAGACCATAACTTG 7094
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 7095 TGTGCTCCGAGCATCCATATGACCGAGGCGGCAATATTATG---GCGCATGTTTCG 7151
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
DB 7152 TATGTTTCAGTCGGGGATGACCAAGCCAGCGGCGGACATTCGCGCGAACAGGCTC 7205

RESULT 13

US-09-103-840A-2/c
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TUBERCULOSIS

FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 2,73e-07 4403765
Score: 189.50 61
Percent Similarity: 43.4% 25
Best Local Similarity: 30.8% 89
Query Match: 19.0% 23
DB: 3 7

US-08-817-997-2_COPY_36_229 (1-194) x US-09-103-840A-2 (1-4403765)

QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGly 27
DB 2225783 GCGGTCGTGCGCGCATCGGATCCGTGTCGACATCCGCGTCGTTTCGCTCGCGC 2225724
QY 28 SerThrGluProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 2225723 AGCATCAGGCTTCGCTTGGC---GAGTCGGTGAGCGTTCGTCGACTCGCTTACC 2225667
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAla 67
DB 2225666 TCGCAA-----GTTGGCGGCGGTCGATTCGGGTCCTACGCG 2225631
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
DB 2225630 GTGAACATACCCAGCAGCAGCTACCGCGGAGCGCGTCAACGGTTCCGATGATCG 2225571
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
DB 2225570 AGCGCCACATCCAGCGCAGCCGTCGCCAGCTGCCCGAACAACAGGATGTGCTGTGGC 2225511
QY 104 TyrSerGlnGlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaValLys 123
DB 2225510 TATTCGAGGTGCGAGCGTCATCGATTGTCACCTCGCGGATCCCGCGGCGGCA 2225451
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 2225450 GATCATGTCCGCGCTGTCGCCCTTTTCGCGAGCCATCCAGTGGTTTCTCCAGCATGTTG 2225391
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 2225390 TGGGCGCGGCGGTGCTGCGCAATCGGTCCGACATCGCTCGCTGTATAGCTCTAAGACCATAACTTG 2225331
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 2225330 TGTGCTCCGAGCATCCATATGACCGAGGCGGCAATATTATG---GCGCATGTTTCG 2225274
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
DB 2225273 TATGTTTCAGTCGGGGATGACCAAGCCAGCGGCGGACATTCGCGCGAACAGGCTC 2225220

RESULT 14

US-09-103-840A-1/c
Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.

Db 774 AACTGGCCCCAGCACCTCGCCGGGGCTATGTCTCGTCGGGCATGGTCAACACAGCGGCT 833

Qy 186 ArgpheLeuArgAspArgIleArg 193

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Db 834 GACTTCGTTGCCGGAAGCTGCAA 857

Search completed: February 5, 2006, 00:07:16
Job time : 1567 secs

Db 1051 CAGCTTGGTAGAACAACTCGCGACGATCTGATCAACGGCAATAGCGCTTCCTGCGCCGAT 1110
Qy 20 AlalleLeuilePheAlaArgGlySerThrGluProGlyAsnMet-GlyIle----- 36
Db 1111 GTCATCTTCAATTATGCGCGAGGTTCAACAGAGACGGGCAACTGGTTGCTAGAAATTTCT 1170
Qy 37 -----ThrValGlyProAlaLeuAl 43
Db 1171 TCTCATGACCAATCATTCTTTCTTACATCATTCATTAGGAACTCTCGGTCCTAGCAATGC 1230
Qy 43 aAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyValGlyGlyPr 61
Db 1231 CTCCAACTTGTAGTTCGCTTCGGCAGACCGTGTCTGATTCAGGGGTTGGCGGTGC 1290
Qy 61 oTyrAspAlaLaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAs 81
Db 1291 CTACGACCACTCTTTGGAGACAATGCTCTCCCTCGCGAACTCTTAGCGCGCAATCAG 1350
Qy 81 pGluGlyIysArgLeuPheAlaLeuAlaAsnGlnIysCysProAsnThrProValValAl 101
Db 1351 GGAGATGCTCGGTCTCTTCCAGCAGGCCAACACCAAGTGCCTCGACGACTTTGATCGC 1410
Qy 101 aGlyGlyTrpSerGlnGlyAlaLeuIleAlaAlaValSerGluLeuSerGlyAl 121
Db 1411 CGTGGCTACACCCAGGGGCTGCACTTCGACCGCTCCCTCGAGGACTTCGACTCGGC 1470
Qy 121 aValIysGluGlnValIysGlyValAlaLeuPheGlyTrpThrGlnAsnLeuGlnAsnAr 141
Db 1471 CATTCGTGACAGATCGCGGAACTGTTCTGTTGGCTACACCAAGAACTACAGAACCG 1530
Qy 141 gGlyGlyIleAlaAsnTyrProArgGluArgThrIysValPheCysAsnValGlyAspAl 161
Db 1531 TGGCCGAATCCCACTACCTCGCGACAGGACCAAGGTCTTCTGCAATACAGGGGATCT 1590
Qy 161 aValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaAr 181
Db 1591 CGTTTGTATCTGTAGTCTGATCGTCTGCTGCACCTCACTTGGCTTATGGTCTGATGCTCG 1650
Qy 181 gGlyGluAlaLaArgPheLeuArgAspArgIleArgAla 194
Db 1651 TGGCCCTGCCCTGAGTTCTCTATCGAGAAGGTTTCGGGCT 1690

RESULT 2

US-10-424-599-33038
; Sequence 33038, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 33038
; LENGTH: 822
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(822)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_129838C.1
US-10-424-599-33038

Alignment Scores:

Pred. No.: 1,08e-24 Length: 822
Score: 268.50 Matches: 74
Percent Similarity: 48.9% Conservative: 19

Best Local Similarity: 38.9% Mismatches: 76
Query Match: 27.0% Indels: 21
DB: 7 Gaps: 8
US-08-817-997-2_COPY_36_229 (1-194) x US-10-424-599-33038 (1-822)
Qy 3 GlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeu 22
Db 244 GGAACACCTACACCAAGCTACCGACGGGACA-----CCTTCCGCCCCGTACATCG 297
Qy 23 IlePheAlaArgGlySerThrGluProGlyAsnMetGly-----IleThrValGlyPro 40
Db 298 GTGTATGCTCAGGAAGTCCAGGATGTAACGTGGAGACCCAGCTGCGTGGCGCG 357
Qy 41 AlaLeuAlaAsnGlyLeuGluSerHisIle-----ArgAsnIleTrpIleGlnGlyVal 58
Db 358 ATCTTCTTCAACAACCTTGGCTCCCGCATCGAGCTGTCCAACTGGCTGTCAGGGTGT 417
Qy 59 GlyGlyProTyrAspAlaLaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAla 78
Db 418 -----CCTTAT-----GCGCGCAACGTTCTC-----GGATACCTCCAGGA 453
Qy 79 AsnIleAspGluGlyIysArgLeuPheAla-----LeuAlaAsnGlnIysCys 94
Db 454 GCGATCCCACTGGCAGCAGCAATGCTGATCTGATCAACCGGCGCCGCAATGC 513
Qy 95 ProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaLaLeuIleAlaAla 114
Db 514 CCCAACACCAAGATTGTTCATCAGCGGCTACAGGCGAGCGGCCAGCTCGTCCACACGCC 573
Qy 115 ValSerGluLeuSerGlyAlaValIysGluGlnValIysGlyValAlaLeuPheGlyTyr 134
Db 574 GCGGCGATGCTCTCTCTCTCCGTGACCAACCGAGTCAACCGAGTGTGTACCTTCGGTGC 633
Qy 135 ThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrIysVal 154
Db 634 CCGAGCGGAACACGACCTTTGGACCAATC-----CCTACAGCCGCGACCGCATC 684
Qy 155 PheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeu 174
Db 685 TTCTGCGTTTCAGGGGACAACTCTGTGATGGCGCATCATCATCCCCCGCGCACACT 744
Qy 175 SerTyrThrIleGluAlaArgGlyGluAla 184
Db 745 CAGTACCAGCAAGACGCGCGCTGCTGCG 774

RESULT 3

US-10-231-478-2
; Sequence 2, Application US/10231478
; Publication No. US20030124683A1
; GENERAL INFORMATION:
; APPLICANT: KAWABE, TOMOYASU
; APPLICANT: KAWITAMARI, MASASHI
; TITLE OF INVENTION: ENZYME PREPARATION AND METHOD OF USING THE SAME
; FILE REFERENCE: 7372/73243
; CURRENT APPLICATION NUMBER: US/10/231,478
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: JP 2001-265495
; PRIOR FILING DATE: 2001-09-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(765)
US-10-231-478-2

Alignment Scores:

Pred. No.: 1.27e-23 Length: 768
Score: 260.00 Matches: 62

Percent Similarity: 50.5% Conservatives: 30
Best Local Similarity: 34.1% Mismatches: 70
Query Match: 26.1% Indels: 20
DB: 6 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-231-478-2 (1-768)

QY 11 SerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGlySerThrGlu 30
Db 229 AATGATTTACTGGTCTGCACGGATTACACCGTTCTCTTCGCCCGCGAACCAGTGAG 288
QY 31 ProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeuGlySerHisIle 50
Db 289 CCGGAAACGTTGGTCTCTCGACCTCTTCTGAGGGGTTGAGGAGCGGTC 348
QY 51 -----ArgAsnLeuTrpIleGlnGlyValGlyProTyAspAlaLeuAlaThr 68
Db 349 GGTGGCGCCGCTTGAGCTTCCAGGGGTGTCACCGC---TATTCTGCATCTGTC---GAG 402
QY 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
Db 403 GGATATTGGCTGGAGGT-----GAAAGCCGCTGGCAGCAAGGCA 441
QY 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
Db 442 ATGGCATCTCAGCGCAGCGACATTCTCCAGGTCTCCGACACCAAGCTTGTATGAGT 501
QY 103 GlyTySerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
Db 502 GGTATTTCCAGGGCTGCCAGATTGTTACAAATGCCGTGAGCACTTCTTCGGGACAC 561
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyThrGlnAsnLeuGlnAsnArgGly 142
Db 562 GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAGGGCAAG 612
QY 143 GlyIleAlaAsnTyProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db 613 GCTCTCCCAACGTTGATGTTCCCGCTCCACACTGTGTGCCACGCTGGAGACACTATT 672
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyThrIleGluAlaArgGly 182
Db 673 TGCAGAACAGCGTTATTATTCTGCCCGCTCACTTGACCTACGCTGTGTGAGTGGCTTCT 732
QY 183 GluAla 184
Db 733 GCGGCT 738

RESULT 4
US-09-999-170-1
; Sequence 1, Application US/09999170
; Publication No. US20030044894A1
; GENERAL INFORMATION:
; APPLICANT: KAWABE, TOMOYASU
; APPLICANT: KISHIMOTO HIRAMINE, KAE
; TITLE OF INVENTION: METHOD FOR STERILIZING TRANSFORMED CELLS
; FILE REFERENCE: 7372/72243
; CURRENT APPLICATION NUMBER: US/09/999,170
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: JP 2000-368180
; PRIOR FILING DATE: 2000-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 798
; TYPE: DNA
; ORGANISM: ASPERGILLUS FLAVUS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(768)
US-09-999-170-1

Alignment Scores: 1.34e-23 Length: 798
Pred. No.: 1.34e-23 Matches: 62
Score: 260.00

Score: 260.00 Matches: 62
Percent Similarity: 50.5% Conservatives: 30
Best Local Similarity: 34.1% Mismatches: 70
Query Match: 26.1% Indels: 20
DB: 6 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-09-999-170-1 (1-798)

QY 11 SerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGlySerThrGlu 30
Db 229 AATGATTTACTGGTCTGCACGGATTACACCGTTCTCTTCGCCCGCGAACCAGTGAG 288
QY 31 ProGlyAsnMetGlyLeuThrValGlyProAlaLeuAlaAsnGlyLeuGlySerHisIle 50
Db 289 CCGGAAACGTTGGTCTCTCGACCTCTTCTGAGGGGTTGAGGAGCGGTC 348
QY 51 -----ArgAsnLeuTrpIleGlnGlyValGlyProTyAspAlaLeuAlaThr 68
Db 349 GGTGGCGCCGCTTGAGCTTCCAGGGGTGTCACCGC---TATTCTGCATCTGTC---GAG 402
QY 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
Db 403 GGATATTGGCTGGAGGT-----GAAAGCCGCTGGCAGCAAGGCA 441
QY 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
Db 442 ATGGCATCTCAGCGCAGCGACATTCTCCAGGTCTCCGACACCAAGCTTGTATGAGT 501
QY 103 GlyTySerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVal 122
Db 502 GGTATTTCCAGGGCTGCCAGATTGTTACAAATGCCGTGAGCACTTCTTCGGGACAC 561
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyThrGlnAsnLeuGlnAsnArgGly 142
Db 562 GCAAGCAAGATCAGCAGCGTCTCTTTTCGGA-----GACCCATACAGGGCAAG 612
QY 143 GlyIleAlaAsnTyProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
Db 613 GCTCTCCCAACGTTGATGTTCCCGCTCCACACTGTGTGCCACGCTGGAGACACTATT 672
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyThrIleGluAlaArgGly 182
Db 673 TGCAGAACAGCGTTATTATTCTGCCCGCTCACTTGACCTACGCTGTGTGAGTGGCTTCT 732
QY 183 GluAla 184
Db 733 GCGGCT 738

RESULT 5
US-10-114-116-2
; Sequence 2, Application US/10114116
; Publication No. US20020164727A1
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Co. Ltd.
; TITLE OF INVENTION: Esterase Genes and Use thereof
; FILE REFERENCE: PI50409
; CURRENT APPLICATION NUMBER: US/10/114,116
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US/09/585,468
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(768)
US-10-114-116-2

Alignment Scores: 1.34e-23 Length: 798
Pred. No.: 1.34e-23 Matches: 62
Score: 260.00

Percent Similarity: 50.5% Conservative: 30
Best Local Similarity: 34.1% Mismatches: 70
Query Match: 26.1% Indels: 20
DB: 5 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-114-116-2 (1-798)

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QY 11 SerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGlySerThrGlu 30
DB 229 AATGGATTACTGGTCCGCGGATTTACACCGTTCTCTTCGCCCGCGAACCAGTGAG 288
QY 31 ProGlyAsnMetGlyThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
DB 289 CCGGAAACGTTGGTCTCGTCGACCTCTCTTCGTCGAGCGGTTGAGGAGCGGTC 348
QY 51 -----ArgAsnIleTrpIleGlnGlyValGlyProGlyProGlyProGlyProGly 68
DB 349 GGTGCGTCCGCTTGGAGCTTCCAGGTTGTCACGGC---TATTCGCACTGTC---GAG 402
QY 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
DB 403 GGATATTGGCTGGAGT-----GAGCGCGTGGCAGCAAGGCA 441
QY 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
DB 442 ATGGCATCTCAGCGCCAGCATTTCTTCCAGTGTCCGACACCAAGCTTGTCTAGT 501
QY 103 GlyTyrSerGlnGlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaVal 122
DB 502 GGTATTCCAGGCGTCCAGATTGTTTCAATGCGGTTGAGCAACTTCTCGCGAACAC 561
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
DB 562 GCAAGCAAGATCAGCAGCGTCTCTCTTTTCGGA-----GACCCATACAAGGCAAG 612
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
DB 613 GCTCTCCCAACGTTGATGTTCCCGCTCCACACTGTGTGCACCGTGGAGACACTATT 672
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
DB 673 TGCAGAACAGCGTTATTATTCTGCGCGCTCACTTGACCTACGCTGTTGATGGCTTCT 732
QY 183 GluAla 184
DB 733 GCGGCT 738
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RESULT 6

US-10-114-115A-2
; Sequence 2, Application US/10114115A
; Publication No. US20020173013A1
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Co. Ltd.
; TITLE OF INVENTION: Esterase Genes and Use thereof
; FILE REFERENCE: P150409
; CURRENT APPLICATION NUMBER: US/10/114,115A
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/585,468
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 798
; TYPE: DNA
; ORGANISM: Aspergillus flavus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(768)
US-10-114-115A-2

Alignment Scores: Length: 798
Pred. No.: 1.34e-23
Score: 260.00
Matches: 62
Conservative: 30
Percent Similarity: 50.5%

Best Local Similarity: 34.1% Mismatches: 70
Query Match: 26.1% Indels: 20
DB: 5 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-114-115A-2 (1-798)

```
QY 11 SerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGlySerThrGlu 30
DB 229 AATGGATTACTGGTCCGCGGATTTACACCGTTCTCTTCGCCCGCGAACCAGTGAG 288
QY 31 ProGlyAsnMetGlyThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIle 50
DB 289 CCGGAAACGTTGGTCTCGTCGACCTCTCTTCGTCGAGCGGTTGAGGAGCGGTC 348
QY 51 -----ArgAsnIleTrpIleGlnGlyValGlyProGlyProGlyProGlyProGly 68
DB 349 GGTGCGTCCGCTTGGAGCTTCCAGGTTGTCACGGC---TATTCGCACTGTC---GAG 402
QY 69 AsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAla 88
DB 403 GGATATTGGCTGGAGT-----GAGCGCGTGGCAGCAAGGCA 441
QY 89 LeuAlaAsnGln-----LysCysProAsnThrProValValAlaGly 102
DB 442 ATGGCATCTCAGCGCCAGCATTTCTTCCAGTGTCCGACACCAAGCTTGTCTAGT 501
QY 103 GlyTyrSerGlnGlyAlaAlaLeuLeuAlaAlaValSerGluLeuSerGlyAlaVal 122
DB 502 GGTATTCCAGGCGTCCAGATTGTTTCAATGCGGTTGAGCAACTTCTCGCGAACAC 561
QY 123 LysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGly 142
DB 562 GCAAGCAAGATCAGCAGCGTCTCTCTTTTCGGA-----GACCCATACAAGGCAAG 612
QY 143 GlyIleAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaVal 162
DB 613 GCTCTCCCAACGTTGATGTTCCCGCTCCACACTGTGTGCACCGTGGAGACACTATT 672
QY 163 CysThrGlyThrLeuIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGly 182
DB 673 TGCAGAACAGCGTTATTATTCTGCGCGCTCACTTGACCTACGCTGTTGATGGCTTCT 732
QY 183 GluAla 184
DB 733 GCGGCT 738
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RESULT 7

US-10-425-115-143033
; Sequence 143033, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 143033
; LENGTH: 874
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(874)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_61927C.1
US-10-425-115-143033

Alignment Scores:
Pred. No.: 5 37e-17 Length: 874
Score: 210.00 Matches: 65
Percent Similarity: 45.4% Conservative: 28
Best Local Similarity: 31.7% Mismatches: 74
Query Match: 21.1% Indels: 38
DB: 8 Gaps: 8

US-08-817-997-2_COPY_36_229 (1-194) x US-10-425-115-143033 (1-874)

QY 7 AsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArg 26
DB 263 AACGAGTACCGAGCGCACC-----GCCTGCGCGCCGATCAGCGTCACTAGCTCGC 316

QY 27 GlySerThrGluProGlyAsnMetGly-----IleThrValGlyProAlaLeuAlaAsn 44
DB 317 GGCACCTCGCAGCGAGCAACGTTGGGACTCGCGCTCCGTTGGCCCTCTGTTCTTCAAC 376

QY 45 GlyLeuGluSerHisle-----ArgAsnIleTrpIleGlnGlyValGlyPro 61
DB 377 CAGATCGCCAGCGCGTGTGCGCGCACCAGCAGCGTCCGATCCAGCGCGCCACGTACCCC 436

QY 62 TyrAspAlaAlaLeuAlaThrAsnPheLeuProArgGly-----ThrSer 76
DB 437 -----GCCAGCTCAGCGGCTTCTTGCTGTGTGTGATGCGCGGAGCAGCACCC 487

QY 77 GlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsn 96
DB 488 ATGACCAAC-----CTCATCAGCAGCAGCGCCACCGCTGCGCCCAAC 529

QY 97 ThrProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuLeuAlaAlaValSer 116
DB 530 ACCAAGATCGTCTCGCGGCTACAGCAGCGCGCGAGCTCGTGCAACCGCGCGGC 589

QY 117 GluLeuSerGlyAlaValLysGlnValLysGlyValAlaLeuPheGlyTyrThrGln 136
DB 590 CGCACCTCGACGCCAACCGCGCAAGTCGCGCGCGTGTGCTGCTTCGCGCGCAAG 649

QY 137 AsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCys 156
DB 650 CGCGGCGAGTCCCTCAGCCCATCGCC-----GCCTCCAGGTCCTCACCATCGC 700

QY 157 AsnValGlyAspAlaValCysThrGlyThrLeuIleThrProAlaHisLeuSerTyr 176
DB 701 CACGACGCGGACAACTCTCGAGGCGGATCGTCCATCACCATCGCCCACTGACTTAC 760

QY 177 ThrIleGluAla-----ArgGly 182
DB 761 CAGATGGATGTCCGCCACCGCGCGCTTTTGTTGCTGTGAAGGTTTAGACACCAAAAAA 820

QY 183 GluAlaAlaArgPhe 187
DB 821 GAGAGAGCGGTTTTT 835

RESULT 8
US-10-425-115-62450/c
; Sequence 62450, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 62450
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Zea mays

FEATURE:
OTHER INFORMATION: Clone ID: MET4577_156956C.1
US-10-425-115-62450

Alignment Scores:
Pred. No.: 1.14e-16 Length: 630
Score: 206.00 Matches: 56
Percent Similarity: 49.4% Conservative: 24
Best Local Similarity: 34.6% Mismatches: 72
Query Match: 20.7% Indels: 10
DB: 8 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-425-115-62450 (1-630)

QY 34 MetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisle-----Arg 51
DB 628 GTCGCGCAGTTGCGAGGACCTCCCTTCTCAAGGCGCTCGGCGAGAAGATTGGCCAGGAC 569

QY 52 AsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeu 71
DB 568 AAGCTCGCGCTTTCAGGCGTT-----GACTACAGCGCCAGCATTTGCT---GGTATTATG 518

QY 72 ProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsn 91
DB 517 CAGATGGGC-----GACAGCGCGCTCTGAGAGATGGCGAGCTTGTCTACGGAGGCTGTT 461

QY 92 GlnLysCysProAsnThrProValValAlaAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIle 111
DB 460 AAGAAGTGCCCAAGACCAAGATCGTCATGTGTGATCTCTCAGGAGCCATGCTGTG 401

QY 112 AlaAlaAlaValSerGluLeuSerGlyAlaValLysGlnValLysGlyValAlaLeu 131
DB 400 CACACGCTGCGCGGCTTCTCTCTGCTGAGACACACAGCGAGGTTGCTCGCGTTCTCAAC 341

QY 132 PheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAsnTyrProArgGluArg 151
DB 340 TTCGCG-----GACCTTTCAGAGACAGCGCATCCAGGCGTCCCGCTGACAGG 290

QY 152 ThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleThrPro 171
DB 289 GTCAGATTATCTGCCAGCGAGCGATGTTGTTGCGCGGTACTGCTGCCATCACCC 230

QY 172 AlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArg 191
DB 229 GACCACCTTACTACAGCAAGATGCT---GCGCGTGTGCTGATTGTTGTTGCGCAAG 173

QY 192 IleArg 193
DB 172 GTGCAA 167

RESULT 9
US-09-894-844-13
; Sequence 13, Application US/09894844
; Patent No. US20020176873A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/09/894,844
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/319,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 651
; TYPE: DNA

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; ORGANISM: Mycobacteria tuberculosis
US-09-894-844-13

Alignment Scores:
Pred. No.: 1-72e-14 Length: 651
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservatives: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-09-894-844-13 (1-651)
QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
Db 76 GCGCGTGTGCGCGCATCGGATCGGTGTTCGACATCGCGTGTTCGCTCGCGGC 135
QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaLeuGlu 47
Db 136 ACGCATCAGGCTTCGCTTGGC---GAGCTCGGTAGGCGTTCGTCGACTCGCTTACC 192
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAla 67
Db 193 TCGCAA-----GTTGGCGGCGGTCTGATTTGGGGTCTACGCG 228
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
Db 229 GTGAACCTACCGACGACGAGCTACCGCGCGGCGGTCAACCGTTCCGATGATCGG 288
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 103
Db 289 AGCGCCACATCCAGCGCACCGTCCGACGCTGCCGACACACAGGATTTGCTTGGTGC 348
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
Db 349 TATTCGAGGTGCGAGCGTCATCGATTGTCACCTCGCGGCGCGCGCGGTGGCA 408
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyThrGlnAsnLeu 138
Db 409 GATCATGTGCGCGCTGTGCGCTTTTCGCGGAGCCATCCAGTGGTTCTCCAGCATGTTG 468
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
Db 469 TGGGCGGCGGCGTGTTCGCAATCGGTCCGATCGGTTCGCTGTATAGCTCTAAGACCAAACTTG 528
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
Db 529 TGTGCTCCGACGATCCAATATGACCGGAGCGGCAATATTATG---GCGCATGTTTCG 585
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192
Db 586 TATGTTTCAGTCGGGGATGACAGCCAGCGCGGACATTCGCGGCGACAGGCTC 639

RESULT 11
US-10-388-902-13
; Sequence 13, Application US/10388902
; Publication No. US20040018574A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; FILE REFERENCE: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/10/388,902
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
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; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-10-647-089-13

Alignment Scores:
Pred. No.: 1.72e-14 Length: 651
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservative: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-647-089-13 (1-651)
QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
DB 76 GCGGTGTCGCGCGCATCGGATCCGTCGTTCGGACATCCGTCGTCGTCGTCGTCGCGC 135
QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 136 AGCATCAGGCTCTCGTCTTGGC---GAGTCGCTGAGCGGTCGTCGACTCGCTTACC 192
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyProTyrAspAlaLeuAla 67
DB 193 TCGCAA-----GTTGGCGGCGGTCGATTCGGGCTACGCG 228
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGly 83
DB 229 GTGAACCTACCAGCAAGCAGCAGCTACCGCGGAGCGGTCACACGGTTCGATGATGCG 288
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGly 103
DB 289 AGCGCCACATCCAGCAGCAGCGTCGCCAGCTGCCGACACACAGGATTTGCTTGGTGC 348
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaVallys 123
DB 349 TATTCGAGGTCGCGATTCATCGGTCATCGATTGTCACCTCGGCGATCCAGTGTTCCTCAGCATGTTG 468
QY 124 GluGlnValGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 409 GATCATGTCGCGCTGTCGCCCTTTTCGGCGAGCATCCAGTGGTTTCCAGCATGTTG 468
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 469 TGGGCGCGCGGTCGTTGTCGACAACTCGTCGCTGATAGCTCTAAGACCAATAACTTG 528
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 529 TGTGCTCCCGAGATCCATATATGACCGAGCGGCGCAATATTATG---GGCATGTTTCG 585
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192
DB 586 TATGTTCACTCGGGATGACAGCCAGCGGCGGACATTCGCGCGCAACAGGCTC 639

RESULT 12
US-09-855-604-258
; Sequence 258, Application US/09855604
; Publication No. US20040214165A1
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: FORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
```



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Qy 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
Db 295 GTGAACACTACCCAGCAAGCAGCACTACCGCGCGCGCGTCAAACCGTTCGATGATGCG 354
Qy 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
Db 355 AGCGGCCACATCCAGCGCACCGTCGCGAGTTCGCCAACAACCGAGATTGTGCTGTGTCG 414
Qy 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
Db 415 TATTCGAGGTGCGAGCGTTCGATGTTTCCACCTCGCGCATCCGCCCGCGGTGGCA 474
Qy 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
Db 475 GATCATGTGCGCGCTGTCGCCCTTTTCGGCGAGCCATCCAGTGTGTTCTCCAGCATGTTG 534
Qy 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
Db 535 TGGGGCGCGGGTGTGTCGCGCAATCGTCCGCTGTATAGCTCTAAGACCATAAACTTG 594
Qy 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
Db 595 TGTGCTCCGAGATCCATATATGACCGGAGCGGCGCAATATTATG---GGCATGTTTCG 651
Qy 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192
Db 652 TATGTTTCACTCGGGATGATCAAGCCAGCGCGGACATTCGCGCGCAACAGGCTC 705

RESULT 15
US-09-855-604-260
; Sequence 260, Application US/09855604
; Publication No. US20050158714A9
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: FORTINOL, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: GOGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; FILE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 260
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(717)
US-09-855-604-260

Alignment Scores:
Pred. No.: 1.98e-14 Length: 720
Score: 189.50 Matches: 61
Percent Similarity: 43.4% Conservative: 25
Best local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 3 Gaps: 7
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US-08-817-997-2_copy_36_229 (1-194) x US-09-855-604-260 (1-720)

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Qy 8 GlyLeuGluSerGlySerAlaAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
Db 142 GCGCGTGTCCGCGCATCGGATCCGTTTCGGACATCGCGGTCTCTTTTCGCTCGCGGC 201
Qy 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
Db 202 AGCATCAGGCTTCGTGCTTGGC---GACGTGCTGAGGCGTTCGTGACACTCGCTTACC 258
Qy 48 SerHisIleArgAsnIleTyrIleGlnGlyValGlyGlyProTyrAspAlaAlaLeuAla 67
Db 259 TCGCAA-----CTTGGCGGCGCTCGATTGGGGTCTACGCG 294
Qy 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
Db 295 GTGAACACTACCCAGCAAGCAGCACTACCGCGCGCGCGTCAAACCGTTCGATGATGCG 354
Qy 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
Db 355 AGCGGCCACATCCAGCGCACCGTCGCGAGTTCGCCAACAACCGAGATTGTGCTGTGTCG 414
Qy 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
Db 415 TATTCGAGGTGCGAGCGTTCGATGTTTCCACCTCGCGCATCCGCCCGCGGTGGCA 474
Qy 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
Db 475 GATCATGTGCGCGCTGTCGCCCTTTTCGGCGAGCCATCCAGTGTGTTCTCCAGCATGTTG 534
Qy 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
Db 535 TGGGGCGCGGGTGTGTCGCGCAATCGTCCGCTGTATAGCTCTAAGACCATAAACTTG 594
Qy 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
Db 595 TGTGCTCCGAGATCCATATATGACCGGAGCGGCGCAATATTATG---GGCATGTTTCG 651
Qy 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgile 192
Db 652 TATGTTTCACTCGGGATGATCAAGCCAGCGCGGACATTCGCGCGCAACAGGCTC 705
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Search completed: February 5, 2006, 01:57:36

Job time : 851 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 5, 2006, 00:19:19 ; Search time 239 Seconds
(without alignments)
680.277 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESGSANACPD.....SYTIARGEAEARFLDRIRA 194

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 6068529 seqs, 419036697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications_NA_New -QFMT=fastac -SUFFIX=p2n.rpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSZ=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abes04
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:

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2:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
3:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
4:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
5:	/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
6:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
7:	/cgn2_6/ptodata/2/pubpna/US12_NEW_PUB.seq:
8:	/cgn2_6/ptodata/2/pubpna/US13_NEW_PUB.seq:
9:	/cgn2_6/ptodata/2/pubpna/US14_NEW_PUB.seq:
10:	/cgn2_6/ptodata/2/pubpna/US15_NEW_PUB.seq:
11:	/cgn2_6/ptodata/2/pubpna/US16_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189.5	19.0	651	8	US-11-143-401-13
2	189.5	19.0	654	8	US-11-052-554A-710
3	120.5	12.1	470	7	US-10-802-796-157
4	91	9.1	420	7	US-10-802-796-496
5	89	8.9	5706	8	US-11-052-554A-519
6	87	8.7	1253	6	US-10-838-616-17
					Sequence 13, Appl
					Sequence 710, App
					Sequence 157, App
					Sequence 496, App
					Sequence 519, App
					Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-11-143-401-13
; Sequence 13, Application US/11143401
; Publication No. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; CURRENT FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-13

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c	8	82.5	8.3	414	7	US-10-467-657-2927	Sequence 2927, Ap
c	9	82	8.2	1093	7	US-10-750-185-27797	Sequence 27797, A
c	10	82	8.2	1093	7	US-10-750-185-27797	Sequence 27797, A
c	11	81	8.1	96988	8	US-11-117-187-196	Sequence 196, App
c	12	80.5	8.1	169047	8	US-11-121-086-15	Sequence 15, Appl
c	13	80	8.0	1188	6	US-10-838-616-25	Sequence 25, Appl
c	14	79.5	8.0	4146	8	US-11-052-554A-522	Sequence 522, App
c	15	79	7.9	445	7	US-10-802-796-75	Sequence 75, Appl
c	16	79	7.9	1893	7	US-10-517-939-41	Sequence 41, Appl
c	17	79	7.9	2196	8	US-11-052-554A-539	Sequence 539, App
c	18	78.5	7.9	2406	8	US-11-052-554A-550	Sequence 550, App
c	19	78.5	7.9	3990	8	US-11-052-554A-520	Sequence 520, App
c	20	78.5	7.9	79528	7	US-10-276-233A-6	Sequence 6, Appli
c	21	78	7.8	153376	8	US-11-121-086-5	Sequence 5, Appli
c	22	78	7.8	172543	8	US-11-121-086-6	Sequence 6, Appli
c	23	77.5	7.8	351	7	US-10-467-657-2929	Sequence 2929, Ap
c	24	77	7.7	879	8	US-11-136-527-2695	Sequence 2695, Ap
c	25	77	7.7	950	7	US-10-750-185-53331	Sequence 53331, A
c	26	77	7.7	950	7	US-10-750-623-53331	Sequence 53331, A
c	27	77	7.7	1725	8	US-11-185-342-2	Sequence 2, Appli
c	28	77	7.7	2210	8	US-11-185-342-1	Sequence 1, Appli
c	29	77	7.7	3301	7	US-10-750-185-42771	Sequence 42771, A
c	30	77	7.7	3301	7	US-10-750-623-42771	Sequence 42771, A
c	31	76.5	7.7	1308	7	US-10-467-657-7577	Sequence 7577, Ap
c	32	76.5	7.7	2837	7	US-10-750-185-54633	Sequence 54633, A
c	33	76.5	7.7	2837	7	US-10-750-623-54633	Sequence 54633, A
c	34	76.5	7.7	116856	8	US-11-143-980-1	Sequence 1, Appli
c	35	76	7.6	333	7	US-10-802-796-723	Sequence 723, App
c	36	76	7.6	2133	8	US-11-143-980-13	Sequence 13, Appl
c	37	76	7.6	5242	7	US-10-750-185-24846	Sequence 24846, A
c	38	76	7.6	5242	7	US-10-750-623-24846	Sequence 24846, A
c	39	76	7.6	116856	8	US-11-143-980-1	Sequence 1, Appli
c	40	75.5	7.6	525	8	US-11-059-222-7	Sequence 7, Appli
c	41	75.5	7.6	525	10	US-11-058-976-7	Sequence 7, Appli
c	42	75.5	7.6	3873	7	US-10-750-185-30606	Sequence 30606, A
c	43	75.5	7.6	3873	7	US-10-750-623-30606	Sequence 30606, A
c	44	75.5	7.6	4983	8	US-11-052-554A-521	Sequence 521, App
c	45	75.5	7.6	6014	8	US-11-102-476-45	Sequence 45, Appl

; PRIOR APPLICATION NUMBER: STRESS-RELATED POLYPEPTIDES IN PLANTS

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 5, 2006, 00:19:19 ; Search time 239 seconds
(without alignments)
680.277 Million cell updates/sec

Title: US-08-817-997-2_COPY_36_229

Perfect score: 996

Sequence: 1 QLGAIENGLESGSANACPD.....SYTIEARGEARFLDRIRA 194

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 6068529 seqs, 419036697 residues

Total number of hits satisfying chosen parameters: 12137058

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOST=abss04
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-NO_WMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : Published Applications NA.New.*

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3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189.5	19.0	651	8 US-11-143-401-13	Sequence 13, Appl
2	189.5	19.0	654	8 US-11-052-554A-710	Sequence 710, App
3	120.5	12.1	470	7 US-10-802-796-157	Sequence 157, App
4	91	9.1	420	7 US-10-802-796-496	Sequence 496, App
5	89	8.9	5706	8 US-11-052-554A-519	Sequence 519, App
6	87	8.7	1253	6 US-10-838-616-17	Sequence 17, Appl

c	7	84.5	8.5	37507	7	US-10-522-037-2	Sequence 2, Appli
c	8	82.5	8.3	414	7	US-10-467-657-2927	Sequence 2927, Ap
c	9	82	8.2	1093	7	US-10-750-185-27797	Sequence 27797, A
c	10	82	8.2	1093	7	US-10-750-185-27797	Sequence 27797, A
c	11	81	8.1	96988	8	US-11-117-187-196	Sequence 196, App
c	12	80.5	8.1	169047	8	US-11-121-086-15	Sequence 15, Appl
c	13	80	8.0	1188	6	US-10-838-616-25	Sequence 25, Appl
c	14	79.5	8.0	4145	8	US-11-052-554A-522	Sequence 522, App
c	15	79	7.9	445	7	US-10-802-796-75	Sequence 75, Appl
c	16	79	7.9	1893	7	US-10-517-939-41	Sequence 41, Appl
c	17	79	7.9	2196	8	US-11-052-554A-539	Sequence 539, App
c	18	78.5	7.9	2406	8	US-11-052-554A-550	Sequence 550, App
c	19	78.5	7.9	3990	8	US-11-052-554A-520	Sequence 520, App
c	20	78.5	7.9	79528	7	US-10-276-233A-6	Sequence 6, Appli
c	21	78	7.8	153376	8	US-11-121-086-5	Sequence 5, Appli
c	22	78	7.8	172543	8	US-11-121-086-6	Sequence 6, Appli
c	23	77.5	7.8	351	7	US-10-467-657-2929	Sequence 2929, Ap
c	24	77	7.7	879	8	US-11-136-527-2695	Sequence 2695, Ap
c	25	77	7.7	950	7	US-10-750-185-5331	Sequence 5331, A
c	26	77	7.7	950	7	US-10-750-623-53331	Sequence 53331, A
c	27	77	7.7	1725	8	US-11-185-342-2	Sequence 2, Appli
c	28	77	7.7	2210	8	US-11-185-342-1	Sequence 1, Appli
c	29	77	7.7	3301	7	US-10-750-185-42771	Sequence 42771, A
c	30	77	7.7	3301	7	US-10-750-623-42771	Sequence 42771, A
c	31	76.5	7.7	1308	7	US-10-467-657-7577	Sequence 7577, Ap
c	32	76.5	7.7	2837	7	US-10-750-185-54633	Sequence 54633, A
c	33	76.5	7.7	2837	7	US-10-750-623-54633	Sequence 54633, A
c	34	76.5	7.7	116856	8	US-11-143-980-1	Sequence 1, Appli
c	35	76	7.6	333	7	US-10-802-796-723	Sequence 723, App
c	36	76	7.6	2133	8	US-11-143-980-13	Sequence 13, Appl
c	37	76	7.6	5242	7	US-10-750-185-24846	Sequence 24846, A
c	38	76	7.6	5242	7	US-10-750-623-24846	Sequence 24846, A
c	39	76	7.6	116856	8	US-11-143-980-1	Sequence 1, Appli
c	40	75.5	7.6	525	8	US-11-059-222-7	Sequence 7, Appli
c	41	75.5	7.6	525	10	US-11-058-976-7	Sequence 7, Appli
c	42	75.5	7.6	3873	7	US-10-750-185-30606	Sequence 30606, A
c	43	75.5	7.6	3873	7	US-10-750-623-30606	Sequence 30606, A
c	44	75.5	7.6	4983	8	US-11-052-554A-521	Sequence 521, App
c	45	75.5	7.6	6014	8	US-11-102-476-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-11-143-401-13
; Sequence 13, Application US/11143401
; Publication No. US20060002953A1
; GENERAL INFORMATION:
; APPLICANT: Behr, Marcel
; APPLICANT: Small, Peter
; APPLICANT: Schoolnik, Gary A.
; APPLICANT: Wilson, Michael A.
; TITLE OF INVENTION: Molecular Differences Between Species of
; TITLE OF INVENTION: the M. Tuberculosis Complex
; FILE REFERENCE: STAN102CON
; CURRENT APPLICATION NUMBER: US/11/143,401
; PRIOR FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: US/10/647,089
; PRIOR FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: US/09/894,844
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/318,191
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/097,936
; PRIOR FILING DATE: 1998-08-25
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Mycobacteria tuberculosis
US-11-143-401-13

Alignment Scores: 1.3e-11 Length: 651
Pred. No.: 189.50 Matches: 61
Score: 189.50
Percent Similarity: 43.4% Conservatives: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 8 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-11-143-401-13 (1-651)

QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
DB 76 GCGGTCGTCGCGCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 135
QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 136 ACGCATCAGGCTTCTGGTCTGGC---GAGTCGCGTGGGCTTCGTCGACTCGCTTACC 192
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAla 67
DB 193 TCGCAA-----GTTGGCGGCGGTCGATTTGGGGTCTACGCG 228
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
DB 229 GTGAACCTACCCAGCAAGCAGACTACCGCGCGCGGTCGAACCGGTTCCGATGATCG 288
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
DB 289 AGCGCCACATCCAGCGCAGCTGCGCCAGCTGCGCGAACCACAGGATTTGCTTGGTGGC 348
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
DB 349 TATTCGAGGTCGCGCGCTCATCGATTTGTCACCTCGCGCATCGCGCGCGGTGGCA 408
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 409 GATCATGTGCGCGCTGCGCCCTTTTCGGCGAGCCATCCAGTGGTTCCTCCAGCATGTTG 468
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 469 TGGGCGCGGTCGTCGCGCAATCGTCCGCTGTATAGTCTTAAGACCAATAACTTG 528
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 529 TGTGCTCCGACGATCCAATATGACCGGAGCGGCAATATTATG---GCGCATGTTGCG 585
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
DB 586 TATGTTTCAGTCGCGGATGACAGCCAGCGCGGACATTCGCGCGAAGAGGCTC 639

RESULT 2
US-11-052-554A-710
; Sequence 710, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 710
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-710

Alignment Scores: 1.31e-11 Length: 654
Pred. No.: 189.50 Matches: 61
Score: 189.50
Percent Similarity: 43.4% Conservatives: 25
Best Local Similarity: 30.8% Mismatches: 89
Query Match: 19.0% Indels: 23
DB: 8 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-11-052-554A-710 (1-654)

QY 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGly 27
DB 76 GCGGTCGTCGCGCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCG 135
QY 28 SerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGlu 47
DB 136 ACGCATCAGGCTTCTGGTCTGGC---GAGTCGCGTGGGCTTCGTCGACTCGCTTACC 192
QY 48 SerHisIleArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAlaLeuAla 67
DB 193 TCGCAA-----GTTGGCGGCGGTCGATTTGGGGTCTACGCG 228
QY 68 ThrAsnPheLeuPro-----ArgGlyThrSerGlnAlaAsnIleAspGluGly 83
DB 229 GTGAACCTACCCAGCAAGCAGACTACCGCGCGCGGTCGAACCGGTTCCGATGATCG 288
QY 84 LysArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGly 103
DB 289 AGCGCCACATCCAGCGCAGCTGCGCCAGCTGCGCGAACCACAGGATTTGCTTGGTGGC 348
QY 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
DB 349 TATTCGAGGTCGCGCGCTCATCGATTTGTCACCTCGCGCATCGCGCGCGGTGGCA 408
QY 124 GluGlnValLysGlyValAlaLeuPhe-----GlyTyrThrGlnAsnLeu 138
DB 409 GATCATGTGCGCGCTGCGCCCTTTTCGGCGAGCCATCCAGTGGTTCCTCCAGCATGTTG 468
QY 139 GlnAsnArgGlyGly-----IleAlaAsnTyrProArgGluArgThrLysValPhe 155
DB 469 TGGGCGCGGTCGTCGCGCAATCGTCCGCTGTATAGTCTTAAGACCAATAACTTG 528
QY 156 CysAsnValGlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSer 175
DB 529 TGTGCTCCGACGATCCAATATGACCGGAGCGGCAATATTATG---GCGCATGTTGCG 585
QY 176 TyrThrIleGluAla---ArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
DB 586 TATGTTTCAGTCGCGGATGACAGCCAGCGCGGACATTCGCGCGAAGAGGCTC 639

RESULT 3
US-10-802-796-157
; Sequence 157, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743

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; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 157
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (331)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (362)
; OTHER INFORMATION: a, t, c or g
US-10-802-796-157

Alignment Scores:
Pred. No.: 0.000518 Length: 470
Score: 120.50 Matches: 41
Percent Similarity: 46.1% Conservative: 12
Best Local Similarity: 35.7% Mismatches: 41
Query Match: 12.1% Indels: 21
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-802-796-157 (1-470)
QY 94 CysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAla-----Leu 110
Db 114 TGC CGGGCCACGAGGTGGTCTCGCGGCTACTCCAGGGTGGCGCGTGCATCGACATC 173
QY 111 IleAlaAlaAla-----ValSerGluLeuSerGlyAlaValLys 123
Db 174 GTCACCGCGCACCACTGCGCGCGCTCGGGTTCCAGCAGCGCTTGC CGCGCGGAC 233
QY 124 GluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGly 143
Db 234 GATCATCATCGCGCGATGCGCTGTTCGGG-----AATCCCTCGCGCGCGCTGGC 284
QY 144 -----IleAlaAsnTyrProArg-----GluArgThrLysValPheCysAsnVal 158
Db 285 GGGCTGATGAGCGCCCTGACCCCTCAATTCGGGTCCAAGACCATCANCCTCTGCAACAAC 344
QY 159 GlyAspAlaValCysThr---GlyThrLeuIleThrProAlaHisLeuSerTyrThr 177
Db 345 GGCAGCCCGATTTGTCNCGACGCCAACCCGG-----TGGCGAGCGCACCTAGGCTAGTG 398
QY 178 IleGluAlaArgGlyGluAlaAlaArgPheLeuArgAspArgIle 192
Db 399 CCGCGGATGACCAACACGAGCGCGCGTTCGTGCGAGCAGGATC 443

RESULT 4
US-10-802-796-496
; Sequence 496, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIEYER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000
; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: US/09/673,476
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: PCT/IB99/00740
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2

; SEQ ID NO 496
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (21)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (23)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (106)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (200)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (272)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (355)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (362)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (413)
; OTHER INFORMATION: a, t, c or g
US-10-802-796-496

Alignment Scores:
Pred. No.: 0.952 Length: 420
Score: 91.00 Matches: 29
Percent Similarity: 43.0% Conservative: 8
Best Local Similarity: 33.7% Mismatches: 31
Query Match: 9.1% Indels: 18
DB: 7 Gaps: 4

US-08-817-997-2_COPY_36_229 (1-194) x US-10-802-796-496 (1-420)
QY 94 CysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAla 113
Db 146 TGC CGGGCCACGAGGTGGTCTCGCGGCTACTCCAGGGTGGCGCGTGCATCNACATC 205
QY 114 AlaValSer-----GluLeuSerGlyAlaValLys 123
Db 206 GTCACCGCGCACCACTGCGCGGCTCGGGTTACGACGCGCTTCCCGCCGCGCGGAC 265
QY 124 GluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGly 143
Db 266 GATCATCATCGCGCGATGCGCTGTTCGGG-----AATCCCTCGCGCGCGCTGGC 316
QY 144 -----IleAlaAsnTyrProArg-----GluArgThrLysValPheCysAsnVal 158
Db 317 GGGCTGATGAGCGCGCTGACCCCTCAATTCGGGTCCAANACCATCNACCTCTGCAACAAC 376
QY 159 GlyAspAlaValCysThr 164
Db 377 GGCAGCCCGATTTGCTTCG 394

RESULT 5
US-11-052-554A-519/c
; Sequence 519, Application US/11052554A
; Publication No. US2005028866A1
; GENERAL INFORMATION:
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; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 519
; LENGTH: 5706
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-519

Alignment Scores:
Pred. No.: 55.8 Length: 5706
Score: 89.00 Matches: 43
Percent Similarity: 41.7% Conservative: 10
Best Local Similarity: 33.9% Mismatches: 62
Query Match: 8.9% Indels: 12
DB: 8 Gaps: 6

US-08-817-997-2_COPY_36_229 (1-194) x US-11-052-554A-519 (1-5706)

Qy 8 GlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeu-----IlePheAla 25
Db 3852 GCGCGCGAATCCGGCGTTCGCCCGCTCCCGCGGATGCGCGCTTGCGCGCCGACCGCC 3793

Qy 26 ArgGlySerThrGluProGlyAsnMetGly---IleThrValGlyProAlaLeuAlaAsn 44
Db 3792 GTCGGGTCCCGCATCAGGTCCCGGGGGCGCGTCACACCGCCCGCGCGTGGCGCC 3733

Qy 45 GlyLeuGluSerHisLeuArgAsnIleTrpIleGlnGlyValGlyGlyProTyrAspAla 64
Db 3732 GCGCCCGCGCGCGCGCTTGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGCGCC 3673

Qy 65 AlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLys 84
Db 3672 GCGTTGGCGGCC-----GTCAAAGCCGGAGGCGCCAGGCC-----GAGACCGGTGGC 3625

Qy 85 ArgLeuPheAlaLeuAlaAsnGlnLysCysProAsnThrProVal---ValAlaGlyGly 103
Db 3624 TCCTCGCGCGCGTAC-----GCCAACACCGCGCTTCCCGCGCGCGCGCG 3577

Qy 104 TyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAlaValLys 123
Db 3576 CTTACCGCGCGCGCGCGCGAAGCGCGCGCCACCACCGAGCGCGCATCGCGCGGTCCCC 3517

Qy 124 GluGlnValLysGlyValAla 130
Db 3516 GCGCGTGC CGCGCGAGCGCGCC 3496

RESULT 6
US-10-838-616-17/c
; Sequence 17, Application US/10838616
; Publication No. US2006008874A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: CREELMAN, Robert A.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; APPLICANT: LIBBY, Jeffrey M
; TITLE OF INVENTION: Plant Transcriptional Regulators of Abiotic Stress
; FILE REFERENCE: MBI-0069CIP
; CURRENT APPLICATION NUMBER: US/10/838,616
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: Stress-Related Polypeptides in Plants
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; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/685,922
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 09/810,836
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: G3451 Predicted polypeptide sequence is orthologous to G867, G9,
US-10-838-616-17

Alignment Scores:
Pred. No.: 11.9 Length: 1253
Score: 87.00 Matches: 51
Percent Similarity: 32.9% Conservative: 24
Best Local Similarity: 22.4% Mismatches: 86
Query Match: 8.7% Indels: 67
DB: 6 Gaps: 9

US-08-817-997-2_COPY_36_229 (1-194) x US-10-838-616-17 (1-1253)

Qy 11 SerGlySerAlaAsnAlaCysProAspAlaIleLeuIlePheAlaArgGlySer-ThrG1 30
Db 1180 TCTTCTTCCATTGCGATCGACCCACTTGCAATATTGTTATGCAACAATAGTATCTGA 1121

Qy 30 uProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisI1 50
Db 1120 ACCGGTAGTTTCAAAATG-----TTAAACCCCAAGAG 1088

Qy 50 eArgAsnIleTrpIle-----GlnGlyValGlyGlyProTyrAspAla---AlaIe 66
Db 1087 CCGAACCATCTGGATCGGTTTCGACACCGGTCCGACCGGTCCGAAACACGCGACCTCGT 1028

Qy 66 uAlaThrAsnPheLeu-----ProArgGlyTh 75
Db 1027 GTTAACAACATTCCTCTCTTCCAATCGATGAAGTGTCTGTCGCGTCCAGTGCACCG 968

Qy 75 rSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysPr 95
Db 967 GTGMAAACAAACCGGTGCACCGCTTCAGATTCTTCTCTTAACGAACCGGTCCCAAC 908

Qy 95 O----- 95
Db 907 TTTGTTAAGACGTAACCTCTGGCTACTGTTCCAATACGAGTAACGAAACCGCACACTTT 848

Qy 96 -----AsnThrProValValAlaGlyGlyTyrSerGlnG1 107
Db 847 CCCTCCAACGTCTTCGAAGTTCAACAAACCGCTTCGCCCGGTCCGCGTCCGCTCAC 788

Qy 107 yAlaAlaLeuIleAlaAlaValSer---GluLeuSerGlyAlaValLysGluGlnVa 126
Db 787 CGCGCTATCGTCTCGCGCTAACCGCTTAGAGCTCTGTAAACGA-----AAGTG 737

Qy 126 lLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGlyIleAlaAs 146
```

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Db 736 CTCTCCGCGTGTCTCGTATCACCAACGGTTC-----AA 698
Qy 146 nTyrProArgGluArgThrIlysValPheCysAsnValGlyAspAlaValCysThrGlyTh 166
Db 697 TTTCCTCA-----ACGTGCGTCCGGGTAACAGCCTTCTCGAATAGCTGCTCACGTGC 647
Qy 166 rLeullelleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAlaAa 186
Db 646 CTTAGTAAACACGCGCCGGAATTTGAGTTTGGGTGCGCGCGCGGAGCCTCGCCG 587
Qy 186 qPheLeuArgAspArgIleArg 193
Db 586 CCGGACGACGCGCGGCTGCGC 565

RESULT 7
US-10-522-037-2/c
; Sequence 2, Application US/10522037
; Publication No. US20050282166A1
; GENERAL INFORMATION:
; APPLICANT: LIBRAGEN
; TITLE OF INVENTION: Method for the expression of unknown environmental DNA into adap
; TITLE OF INVENTION: cells.
; FILE REFERENCE: B0149W0
; CURRENT APPLICATION NUMBER: US/10/522,037
; CURRENT FILING DATE: 2005-01-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 37507
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: DNA sequence of clone FS3-135.
US-10-522-037-2

Alignment Scores:
Pred. No.: 2,33e+03 Length: 37507
Score: 84.50 Matches: 51
Percent Similarity: 42.0% Conservative: 22
Best Local Similarity: 29.3% Mismatches: 68
Query Match: 8.5% Indels: 34
DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-522-037-2 (1-37507)

Qy 25 AlaArgGlySerThrGluProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsn 44
Db 21962 GCGCGGGCGCGCTCGATGTCGCGGAGTGGCGCGCTTCATCGCTCGCGCTGCA--- 21906
Qy 45 GlyLeuGluSerHisIleArgAsnIleTrieGlnGlyValGlyGlyProTyrAspAla 64
Db 21905 -----CCGCGTTTCGGGTGACGAGAGCGCGCGCTGC- GTGCGCGCCC 21865
Qy 65 AlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIleAspGlyLys 84
Db 21864 GCGCGCTCGCGCGGTGATCCCGCGCGC---TCTCGCGCAACATTCGTGCTCG- 21811
Qy 85 ArgLeuPheAlaLeuAlaGlnLysCysProAsn-----ThrPro-ValValAlaG1 102
Db 21810 -----GCGAATCGTCTGATGCGGCTGCGCGCTCGCGCTCGCGCGC 21766
Qy 102 yGlyTyrSerGlnGlyAlaAlaLeuIleAlaAlaValSerGluLeuSerGlyAla 122
Db 21765 AGGGTTGCGCGAGGTGCGCACCGCGGTGTCGCGCGGTTCGCGAGCGTCCGCGCA-- 21708
Qy 122 lLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgG1 142
Db 21707 -----CGCGCGGAGGGAACCTGTTGTGGCGCGCTCCCGCTCCGGGGGCGACG 21655
Qy 142 yGlyIleAlaAsnTyrProArgGluArgThrIlysValPheCysAsnValGlyAspAla 162
Db 21654 CAAGCGCGAGGTGCGCGCGCTCGA----- 21627
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Qy 162 lCysThrGlyThrLeullelleThrProAla-HisLeuSerTyrThrIleGluAlaArg 182
Db 21626 -TGC CGCGCGCTTCGTTCCTGAGACCCACTACACGCGCGCGCTGCGCGCTCGCGCGC 21568
Qy 182 lYGuAlaAlaArgPheLeuArgAspArgIleArgAla 194
Db 21567 GCGAGCTGCG---ATGCTGCGCGATTGCTCGCGCGCC 21533

RESULT 8
US-10-467-657-2927
; Sequence 2927, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2927
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2927

Alignment Scores:
Pred. No.: 8.51 Length: 414
Score: 82.50 Matches: 36
Percent Similarity: 44.6% Conservative: 18
Best Local Similarity: 29.8% Mismatches: 36
Query Match: 8.3% Indels: 31
DB: 7 Gaps: 8

US-08-817-997-2_COPY_36_229 (1-194) x US-10-467-657-2927 (1-414)

Qy 27 GlySerThrGluProGlyAsnMetGlyIleThrValGly----- 39
Db 55 GGTTCCTCAAAGGCGGGAATGCTGTTCTTCTTGTGCGTGCAGATTCTTGTGCGCTCC 114
Qy 40 -----ProAla---LeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrieGln 56
Db 115 GGGCAACACGCGCAAAATTGAAACGCGTGCATCCAGCGCTCCGGAATATATTGCTTCAG 174
Qy 57 GlyVal-----GlyGlyProTyrAspAlaAlaLeuAlaThrAsnPheLeuPro 72
Db 175 GTTTTCATGTCGTCACAGATGAGCGGTACATTGCT-----GTAACTGCTTCCTG--- 225
Qy 73 ArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGln 92
Db 226 -----CAGACGGCATCGGTGTTGTTTCAGGGCTTCGGCTG-----GATGTC 267
Qy 93 LysCysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAlaLeuIleAla 112
Db 268 GAATGCCACACTTTCCTCCCTGTTGCGTGGTTCGCGAGGAAAGGGTGTGCGTGC 327
Qy 113 AlaAlaValSerGluLeuSerGlyAlaValLysGluGlnValLysGlyValAlaLeuPhe 132
Db 328 GTTGGC-----GGCGGTGCGCTCCAGCGC-----ATTGCCGCTTC 363
Qy 133 Gly 133
Db 364 GGG 366

RESULT 9
US-10-750-185-27797/c
```

; Sequence 27797, Application US/10750185
 ; Publication No. US20050260603A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10750,185
 ; PRIOR FILING DATE: 2003-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; PRIOR FILING DATE: 2002-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27797
 ; LENGTH: 1093
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880669084
 ; US-10-750-185-27797

Alignment Scores:
 Pred. No.: 36.3 Length: 1093
 Score: 82.00 Matches: 45
 Percent Similarity: 40.9% Conservative: 27
 Best Local Similarity: 25.6% Mismatches: 66
 Query Match: 8.2% Indels: 38
 DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-750-185-27797 (1-1093)

```

Qy 35 GlyIleThrValGlyProAlaLeuAla---AsnGlyLeuGluSerHisIleArgAsn--- 52
Db 579 GGGACTGTCTCGTCCCTCCCTCGGCGCTGAGGGGCTGCAGAGTGCCTGAAGAGGGT 520
Qy 53 -----IleTrpIleGlnGlyValGlyGlyPro-TyrAspAlaAlaLeuAlaTh 68
Db 519 CCCACGTGCTGGACTGGCCCCAAGGCTGCAGGACCTTGGCCACTGCCGCCACCCTC 460
Qy 68 rAnPheLeu---ProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPh 87
Db 459 CCAGTTCTTCAGCCCTCTGTGGCGGCCCCAGGCCAACCTGTAGGAGGAGTGCCTCT 400
Qy 87 eAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGlnG 107
Db 399 GGGTTGGTGGCAGAG-----GTGGTCTGTGGC-----CAGGG 367
Qy 107 yAlaAlaLeuIleAlaAlaValSerGluLeuSerGly----- 120
Db 366 GGCTGTCTGTGGCGCAGACTGTGGCCAGCTTCCAGACGCCAAGCTGTTCTGTCCAGTT 307
Qy 121 ----AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuG 139
Db 306 GTTGGCTGACGCTGCGCAGCTAGGAGTCTGAATGCCATCCAGCAGGAAGAGCAGC 247
Qy 139 nAnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCys----- 156
Db 246 ATCTGTAGTTCGACTCCGGGACTTCCAGAAATGAAGGAAGCATGTGCTTCTTGTG 187
Qy 157 -----AsnValGlyAspAlaValCysThrGlyThrLe 167
Db 186 GAGCCTTGTCCCTTTCCTGTAGTGGGTGAAGTGGGTTCAGTCACTTCCAAAAATATTTT 127
Qy 167 uile-IleThrProAlaHisLeuSerTyrThrIleGluAlaArg 181
Db 126 AGTGTCTATTTCCCGCAGTCACTGAACACACACTTGAGGGGTAGA 83

```

RESULT 10
 US-10-750-623-27797/c
 ; Sequence 27797, Application US/10750623

; Publication No. US20050287531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-1
 ; CURRENT APPLICATION NUMBER: US/10750,623
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIOR FILING DATE: 2002-12-31
 ; PRIOR APPLICATION NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27797
 ; LENGTH: 1093
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880669084
 ; US-10-750-623-27797

Alignment Scores:
 Pred. No.: 36.3 Length: 1093
 Score: 82.00 Matches: 45
 Percent Similarity: 40.9% Conservative: 27
 Best Local Similarity: 25.6% Mismatches: 66
 Query Match: 8.2% Indels: 38
 DB: 7 Gaps: 7

US-08-817-997-2_COPY_36_229 (1-194) x US-10-750-623-27797 (1-1093)

```

Qy 35 GlyIleThrValGlyProAlaLeuAla---AsnGlyLeuGluSerHisIleArgAsn--- 52
Db 579 GGGACTGTCTCGTCCCTCCCTCGGCGCTGAGGGGCTGCAGAGTGCCTGAAGAGGGT 520
Qy 53 -----IleTrpIleGlnGlyValGlyGlyPro-TyrAspAlaAlaLeuAlaTh 68
Db 519 CCCACGTGCTGGACTGGCCCCAAGGCTGCAGGACCTTGGCCACTGCCGCCACCCTC 460
Qy 68 rAnPheLeu---ProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPh 87
Db 459 CCAGTTCTTCAGCCCTCTGTGGCGGCCCCAGGCCAACCTGTAGGAGGAGTGCCTCT 400
Qy 87 eAlaLeuAlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGlnG 107
Db 399 GGGTTGGTGGCAGAG-----GTGGTCTGTGGC-----CAGGG 367
Qy 107 yAlaAlaLeuIleAlaAlaValSerGluLeuSerGly----- 120
Db 366 GGCTGTCTGTGGCGCAGACTGTGGCCAGCTTCCAGACGCCAAGCTGTTCTGTCCAGTT 307
Qy 121 ----AlaValLysGluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuG 139
Db 306 GTTGGCTGACGCTGCGCAGCTAGGAGTCTGAATGCCATCCAGCAGGAAGAGCAGC 247
Qy 139 nAnArgGlyGlyIleAlaAsnTyrProArgGluArgThrLysValPheCys----- 156
Db 246 ATCTGTAGTTCGACTCCGGGACTTCCAGAAATGAAGGAAGCATGTGCTTCTTGTG 187
Qy 157 -----AsnValGlyAspAlaValCysThrGlyThrLe 167
Db 186 GAGCCTTGTCCCTTTCCTGTAGTGGGTGAAGTGGGTTCAGTCACTTCCAAAAATATTTT 127
Qy 167 uile-IleThrProAlaHisLeuSerTyrThrIleGluAlaArg 181
Db 126 AGTGTCTATTTCCCGCAGTCACTGAACACACACTTGAGGGGTAGA 83

```

RESULT 11
 US-11-117-187-196/c
 ; Sequence 196, Application US/11117187
 ; Publication No. US20050266560A1

```
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPEHAEVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 196
; LENGTH: 96988
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-196

Alignment Scores:
Pred. No.: 2,11e+04 Length: 96988
Score: 81.00 Matches: 25
Percent Similarity: 47.9% Conservative: 10
Best Local Similarity: 34.2% Mismatches: 20
Query Match: 8.1% Indels: 18
DB: 8 Gaps: 2

US-08-817-997-2_COPY_36_229 (1-194) x US-11-117-187-196 (1-96988)

Qy 47 GluSerHisIleArgAsnIleThrPleGlnGlyValGlyGlyProTyr----- 62
Db 80971 GAGAGCTAACTCAATCATCTTCTACAAAGGATAGACAGCCATACGATTCAACTT 80912
Qy 63 AspAlaAlaLeuAlaThrAsnPheLeuProArgGlyThrSerGlnAlaAsnIle----- 80
Db 80911 GATGACAGAGCTCTGTAACTTCTGACAGAGACCACTAGTGAAGCATTAATCTTATC 80852
Qy 81 -----AspGluGlyLysArgLeuPheAla 88
Db 80851 ACCAATGCTTTAACTGCTCATTGCGAGCTAGTAAATTGCAAGAAAGCAAGAAATTCAGCT 80792
Qy 89 LeuAlaAsnGlnLysCysProAsnThrProValValala 101
Db 80791 GAGAAAGCTACCAAGTGCAGAAAGAGACTCATGTTTCAGCA 80753

RESULT 12
US-11-121-086-15/c
; Sequence 15, Application US/11/121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 169047
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-15

Alignment Scores:
Pred. No.: 5,13e+04 Length: 169047
Score: 80.50 Matches: 35
Percent Similarity: 47.2% Conservative: 16
Best Local Similarity: 32.4% Mismatches: 38
Query Match: 8.1% Indels: 20
DB: 8 Gaps: 7
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US-08-817-997-2_COPY_36_229 (1-194) x US-11-121-086-15 (1-169047)

Qy 4 AlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIleLeuIle 23
Db 58404 GCCACAAAGACAGAGGCTTCC-ACTGGCACCTCTCACCCCTCCCTGCTCCCTCTCG 58346
Qy 24 PheAlaArgGlySer---ThrGluProGlyAsnMetGly-----Ile 36
Db 58345 GGTGCACCTGGCTCTTTGGCCCTCTCTGGAGGTAGGATGGCCCTTCGGGGCTGTGTGTG 58286
Qy 37 ThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIle-----Tip 54
Db 58285 CTCITGGGACAGCGGCTCTGCAGATCCCTCGAGCCACACACACGCGACTCTGCGAGTGG 58226
Qy 55 IleGlnGlyVal-----GlyGlyProTyrAspAlaAlaLeuAlaThrAsnPhe 70
Db 58225 GAGCTTGGCACCCGCCAGCACCAAGTGCACACTACCATGTGTCTCTAGCAGAG----- 58172
Qy 71 LeuProArgGlyThrSer---GlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeu 89
Db 58171 CTCCCTACTGGGAGCATGTAAAGGAAATAACAACCAAGGC-----TTTGCCATA 58121
Qy 90 AlaAsnGlnLysCysProAsnThr 97
Db 58120 AGCAATGTAAATGTCCAACCTCC 58097

RESULT 13
US-10-838-616-25/c
; Sequence 25, Application US/10838616
; Publication No. US2006000874A1
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: CREELMAN, Robert A.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: KUMIMOTO, Roderick W
; APPLICANT: GUTTERSON, Neal I
; APPLICANT: REUBER, T. Lynne
; APPLICANT: LIBBY, Jeffrey M
; TITLE OF INVENTION: Plant Transcriptional Regulators of Abiotic Stress
; FILE REFERENCE: MBI-0069CIP
; CURRENT APPLICATION NUMBER: US/10/838,616
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: Stress-Related Polypeptides in Plants
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 10/685,922
; PRIOR FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 09/810,836
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 10/412,699
; PRIOR FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 09/532,591
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,029
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/533,392
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 60/125,814
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/713,994
; PRIOR FILING DATE: 2000-11-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 1188
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: G3454 Predicted polypeptide sequence is orthologous to G867
US-10-838-616-25
```

Alignment Scores:

Pred. No.: 68.4 Length: 1188
Score: 80.00 Matches: 50
Percent Similarity: 31.7% Conservatives: 23
Best Local Similarity: 21.7% Mismatches: 86
Query Match: 8.0% Indels: 71
DB: 6 Gaps: 9

US-08-817-997-2_COPY_36_229 (1-194) x US-10-838-616-25 (1-1188)

Qy 11 SerGlySerAlaAsnAlaCysProAspAlaLeuLeuPheAlaArgGlySer-ThrGl 30
Db 1128 TCTCTCTGTCATGAGCAGCCACTTGCATTATTGTTATGCGCAACATAGTATCTGA 1069
Qy 30 uProGlyAsnMetGlyIleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisI 50
Db 1068 ACCGGGTAGTTTCAAAATG-----TTAACCACCAAGAG 1036
Qy 50 eArgAsnIleTrpIle-----GlnGlyValGlyGlyProTyrAspAla---AlaLe 66
Db 1035 CCGAACCATCTGATCGGTTTCGACAAACCGTTCGACCGGTCCGAACACGACCTCGTT 976
Qy 66 uAlaThrAsnPheLeu-----ProArgGlyTh 75
Db 975 GTTAAACACATCTCTCGTCTTCAATCGATGTAAAGCTGTTCGCGTCCAGTGGACCG 916
Qy 75 rSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeuAlaAsnGlnLysCysPr 95
Db 915 GTGAAAAACAAACCGTGTACACAGCTTTCAGATTCCTTCTTAACGAACCGGCTCCAAAC 856
Qy 95 o----- 95
Db 855 TTTGGTTAAGACGTAACCTCTGCTACTGTGTTTCAATACGAGTAACGAAACCGCACACTTT 796
Qy 96 -----AenThrProValValAlaGlyGlyTyrSerGlnGl 107
Db 795 CCCTCCAAACGCTCTTCGAAGTTCAACAAACGCGCTTCGCGCGTCCGCGCTCAC 736
Qy 107 yAlaAlaLeuIleAlaAlaValSer---GluLeuSerGlyAlaValLysGluGlnVa 126
Db 735 CGCGCGTATCTGTCGCGCTAAGCGCTTAGAGCTCTGTAAACGGA-----AAGTG 685
Qy 126 lLysGlyValAlaLeuPheGlyTyrThrGln-----AsnLeuGlnAsnArgGlyGlyI 144
Db 684 CTCTCCGCGTGTCTGCTTCGGTATCACCACAAACGGTTCAATTCCAAACGTCGCTCGG 625
Qy 144 eAlaAsnTyrProArgGluArgThrLysValPheCysAsnValGlyAspAlaValCysTh 164
Db 624 AACAGCTTTCTCGAATAGC-----TGCTC 601
Qy 164 rGlyThrLeuIleIleThrProAlaHisLeuSerTyrThrIleGluAlaArgGlyGluAl 184
Db 600 ACCTGATTAGTAAAGACACGCGCGGAATTTAGTCTGCGGTGCCGACGCGCGGAGGCC 541
Qy 184 aAlaArgPheLeuArgAspArgIleArg 193
Db 540 TCAGCGCGCGACGACGCGCGGTGCGC 513

RESULT 14

US-11-052-554A-522/c
; Sequence 522, Application US/11052554A
; Publication No. US20050298866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004

; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 522
; LENGTH: 4146
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-522

Alignment Scores:

Pred. No.: 427 Length: 4146
Score: 79.50 Matches: 47
Percent Similarity: 35.4% Conservatives: 17
Best Local Similarity: 26.0% Mismatches: 66
Query Match: 8.0% Indels: 51
DB: 8 Gaps: 10

US-08-817-997-2_COPY_36_229 (1-194) x US-11-052-554A-522 (1-4146)

Qy 2 LeuGlyAlaIleGluAsnGlyLeuGluSerGlySerAlaAsnAlaCysProAspAlaIle 21
Db 2235 CTGGCCGCGCGCCCGCGCATTCGCCCTTCGCCCGCGCGCCACCGCTCGCCGCGTC 2176
Qy 22 LeuIlePheAlaArgGlySerThrGluProGlyAsnMet-----Gly 35
Db 2175 TCCACCTTTGGCGCGCGTGCC-----CCCGCAGGCTCTGTGCCAGTCCCGCGTATGCC 2122
Qy 36 IleThrValGlyProAlaLeuAlaAsnGlyLeuGluSerHisIleArgAsnIleTrpIle 55
Db 2121 GTTCCGCGCGGCC-----GCCAATGCTCCCGCACCGCGTCAACGCCATTACCACC 2068
Qy 56 Gln-----GlyValGlyGlyProTyrAspAlaLeuAlaLeuAlaThrAsn 69
Db 2067 GCTGCGCGCGGTTCCGCTATTCGCGCGCGCGCGCTACGCGCGCTTGGCACCGGC 2008
Qy 70 PheLeuProArgGlyThrSerGlnAlaAsnIleAspGluGlyLysArgLeuPheAlaLeu 89
Db 2007 -----GCCCGCGCTGAAGCGCGC-----TTGCGCGTC 1981
Qy 90 AlaAsnGlnLysCysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAla 109
Db 1980 CAC-----CCCAAGTTGCGCTGTTGCC-----GGTGGCAGC 1948
Qy 110 LeuIleAlaAlaValSerGluLeuSerGlyAlaValLysGluGlnValLysGlyVal 129
Db 1947 CTTGCGCGCGCGGTTGCTG 1888
Qy 130 AlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyLysIleAlaAsnTyrProArg 149
Db 1887 GCTGCC-----CGCGGTGCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCG 1855
Qy 150 GluArgThrLysValPheCysAsnValGlyAspAlaValCysThrGlyThrLeuIleIle 169
Db 1854 -----TGCAGCG 1813
Qy 170 Thr 170
Db 1812 ACC 1810

RESULT 15

US-10-802-796-75
; Sequence 75, Application US/10802796
; Publication No. US20050250104A1
; GENERAL INFORMATION:
; APPLICANT: COLE, STEWART
; APPLICANT: BUCHRIESER-BROSCH, ROLAND
; APPLICANT: GORDON, STEPHEN
; APPLICANT: BILLAULT, ALAIN
; TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
; TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
; TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIA.
; FILE REFERENCE: 05394.0011-00000

; CURRENT APPLICATION NUMBER: US/10/802,796
; CURRENT FILING DATE: 2004-03-18
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; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 75
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-802-796-75

Alignment Scores:

Pred. No.:	23.3	Length:	445
Score:	79.00	Matches:	35
Percent Similarity:	45.9%	Conservative:	10
Best Local Similarity:	35.7%	Mismatches:	34
Query Match:	7.9%	Indels:	21
DB:	7	Gaps:	6

US-08-817-997-2_COPY_36_229 (1-194) x US-10-802-796-75 (1-445)

QY	94	CysProAsnThrProValValAlaGlyGlyTyrSerGlnGlyAlaAla-----Leu	110
DB	153	TGCCGGGCCACGAGGTGGTGTCTCGCGGCTACTCCAGGGTGGCGCGGTGATCGACATC	212
QY	111	IleAlaAlaAla-----ValSerGluLeuSerGlyAlaValLys	123
DB	213	GTCAACGCGCCACCACTGCCCGGCTCGGGTTCACGCAGCGCTTGCCTCCGCGCAGCGGAC	272
QY	124	GluGlnValLysGlyValAlaLeuPheGlyTyrThrGlnAsnLeuGlnAsnArgGlyGly	143
DB	273	GATCATCGCCGCGATCGCCCTGTTCGGG-----AATCCCTCGGGCGCGCTGGC	323
QY	144	-----IleAlaAsnTyrProArgGluArgThrLys-----ValPheCysAsnVal	158
DB	324	GGGCTGATGAGCGCCCTGACCCCTCAATTCCGGTCCAGAACATCAACCTCTGCACCAAC	383
QY	159	GlyAspAlaValCysThrGlyThrLeuIleIleThrProAlaHisLeuSerTyr	176
DB	384	GGCGACCC-ATTGTTC-GGACGCAACCGGTGGCA---ACGCACCTTAAGCTAC	432

Search completed: February 5, 2006, 00:35:34
Job time : 268 secs